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PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

<110> Lindquist, et al.

<120> RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS AND METHODS COMPRISING SAME

<130> 30554/34978A

<150> US 09/591,632
<151> 2000-06-09

<150> US 60/138,833
<151> 1999-06-09

<160> 70

<170> PatentIn version 3.3

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acacacatac atacatttat atttataata agcgttaaaa tttcggcaga atatctgtca 240

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cgctatttga ctcaaattat tatttttac taagacgacg cgtcacagtg ttcgagtctg 360

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catacagaag ttattgtcac ttcttacctt gctcttaaat gtacattaca accgggtatt 540

atatcttaca tcatcgtata atatgatctt tctttatgga gaaaattttt ttttcactcg 600

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actccattgt actgtaacaa aaagcggttt cttcatcgac ttgctcggaa taacatctat 720

atctgcccac tagcaaca atg tcg gat tca aac caa ggc aac aat cag caa 771
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln
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aac tac cag caa tac agc cag aac ggt aac caa caa caa ggt aac aac 819
Asn Tyr Gln Gln Tyr Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn
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aga tac caa ggt tat caa gct tac aat gct caa gcc caa cct gca ggt 867

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tat caa cag tac aat ccc gac gcc ggt tac cag caa cag tat aat cct      963
Tyr Gln Gln Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro
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caa gga ggc tat caa cag tac aat cct caa ggc ggt tat cag cag caa     1011
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Phe Asn Pro Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn
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aac aat ttg caa gga tat caa gct ggt ttc caa cca cag tct caa ggt     1107
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atg tct ttg aac gac ttt caa aag caa caa aag cag gcc gct ccc aaa     1155
Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys
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cca aag aag act ttg aag ctt gtc tcc agt tcc ggt atc aag ttg gcc     1203
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Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys
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gag gaa gag aag tct gct gaa acc aaa gaa cca act aaa gag cca aca     1299
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Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu
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gat gcc ttg atc aag gaa cag gaa gaa gaa gtg gat gac gaa gtt gtt     1491
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Tyr Phe Glu Thr Glu Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly
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His Lys Met Tyr Val Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp
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Phe Glu Arg Gly Gly Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr
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acc gtt aac tgg tct aag gaa cgt tac gac caa tgt gtg agt aat gtc     2019
Thr Val Asn Trp Ser Lys Glu Arg Tyr Asp Gln Cys Val Ser Asn Val
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agc aat ttc ttg aga gca att ggt tac aac att aag aca gac gtt gta     2067
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gat cca aaa gaa tgc cca tgg tac acc ggc cca act ctg tta gaa tat     2163
Asp Pro Lys Glu Cys Pro Trp Tyr Thr Gly Pro Thr Leu Leu Glu Tyr
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ctg gat aca atg aac cac gtc gac cgt cac atc aat gct cca ttc atg     2211
Leu Asp Thr Met Asn His Val Asp Arg His Ile Asn Ala Pro Phe Met
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Lys Ile Glu Ser Gly His Ile Lys Lys Gly Gln Ser Thr Leu Leu Met
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cct aac aaa acc gct gtg gaa att caa aat att tac aac gaa act gaa     2355
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Ala Glu
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Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
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Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln
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Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro Gln Gly
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Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly
100 105 110

Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu Asn Asp
115 120 125

Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu
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Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys
145 150 155 160

Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser
165 170 175

Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu Glu Pro
180 185 190

Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr Glu Glu
195 200 205

Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu Ser Thr
210 215 220

His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu Ile Lys
225 230 235 240

Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp Met Phe Gly

245 250 255

Gly Lys Asp His Val Ser Leu Ile Phe Met Gly His Val Asp Ala Gly
260 265 270

Lys Ser Thr Met Gly Gly Asn Leu Leu Tyr Leu Thr Gly Ser Val Asp
275 280 285

Lys Arg Thr Ile Glu Lys Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg
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Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly Phe Glu Arg Gly Gly
370 375 380

Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr Gln Gly Val Asn Lys
385 390 395 400

Met Val Val Val Val Asn Lys Met Asp Asp Pro Thr Val Asn Trp Ser
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Ala Ile Gly Tyr Asn Ile Lys Thr Asp Val Val Phe Met Pro Val Ser
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Gly Tyr Ser Gly Ala Asn Leu Lys Asp His Val Asp Pro Lys Glu Cys
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Pro Trp Tyr Thr Gly Pro Thr Leu Leu Glu Tyr Leu Asp Thr Met Asn
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His Val Asp Arg His Ile Asn Ala Pro Phe Met Leu Pro Ile Ala Ala
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Lys Met Lys Asp Leu Gly Thr Ile Val Glu Gly Lys Ile Glu Ser Gly
500 505 510

His Ile Lys Lys Gly Gln Ser Thr Leu Leu Met Pro Asn Lys Thr Ala
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Val Glu Ile Gln Asn Ile Tyr Asn Glu Thr Glu Asn Glu Val Asp Met
530 535 540

Ala Met Cys Gly Glu Gln Val Lys Leu Arg Ile Lys Gly Val Glu Glu
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Glu Asp Ile Ser Pro Gly Phe Val Leu Thr Ser Pro Lys Asn Pro Ile
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Lys Ser Val Thr Lys Phe Val Ala Gln Ile Ala Ile Val Glu Leu Lys
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Ser Ile Ile Ala Ala Gly Phe Ser Cys Val Met His Val His Thr Ala
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Ile Glu Glu Val His Ile Val Lys Leu Leu His Lys Leu Glu Lys Gly
610 615 620

Thr Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe Ala Lys Lys Gly Met
625 630 635 640

Lys Val Ile Ala Val Leu Glu Thr Glu Ala Pro Val Cys Val Glu Thr
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  1               5                  10                  15

cgt caa gta aac ata gga aac agg aac agt aat aca acc acc gat caa     277
Arg Gln Val Asn Ile Gly Asn Arg Asn Ser Asn Thr Thr Thr Asp Gln
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agt aat ata aat ttt gaa ttt tca aca ggt gta aat aat aat aat aat     325
Ser Asn Ile Asn Phe Glu Phe Ser Thr Gly Val Asn Asn Asn Asn Asn
        35                  40                  45

aac aat agc agt agt aat aac aat aat gtt caa aac aat aac agc ggc     373
Asn Asn Ser Ser Ser Asn Asn Asn Asn Val Gln Asn Asn Asn Ser Gly
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cgc aat ggt agc caa aat aat gat aac gag aat aat atc aag aat acc     421
Arg Asn Gly Ser Gln Asn Asn Asp Asn Glu Asn Asn Ile Lys Asn Thr
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Leu Glu Gln His Arg Gln Gln Gln Gln Ala Phe Ser Asp Met Ser His
                85                  90                  95

gtg gag tat tcc aga att aca aaa ttt ttt caa gaa caa cca ctg gag     517
Val Glu Tyr Ser Arg Ile Thr Lys Phe Phe Gln Glu Gln Pro Leu Glu
            100                 105                 110

gga tat acc ctt ttc tct cac agg tct gcg cct aat gga ttc aaa gtt     565
Gly Tyr Thr Leu Phe Ser His Arg Ser Ala Pro Asn Gly Phe Lys Val
        115                 120                 125

gct ata gta cta agt gaa ctt gga ttt cat tat aac aca atc ttc cta     613
Ala Ile Val Leu Ser Glu Leu Gly Phe His Tyr Asn Thr Ile Phe Leu
    130                 135                 140

gat ttc aat ctt ggc gaa cat agg gcc ccc gaa ttt gtg tct gtg aac     661
Asp Phe Asn Leu Gly Glu His Arg Ala Pro Glu Phe Val Ser Val Asn
145                 150                 155                 160

cct aat gca aga gtt cca gct tta atc gat cat ggt atg gac aac ttg     709
Pro Asn Ala Arg Val Pro Ala Leu Ile Asp His Gly Met Asp Asn Leu
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tct att tgg gaa tca ggg gcg att tta tta cat ttg gta aat aaa tat     757
Ser Ile Trp Glu Ser Gly Ala Ile Leu Leu His Leu Val Asn Lys Tyr
            180                 185                 190

tac aaa gag act ggt aat cca tta ctc tgg tcc gat gat tta gct gac     805
Tyr Lys Glu Thr Gly Asn Pro Leu Leu Trp Ser Asp Asp Leu Ala Asp
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caa tca caa atc aac gca tgg ttg ttc ttc caa acg tca ggg cat gcg     853
Gln Ser Gln Ile Asn Ala Trp Leu Phe Phe Gln Thr Ser Gly His Ala
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cca atg att gga caa gct tta cat ttc aga tac ttc cat tca caa aag     901
Pro Met Ile Gly Gln Ala Leu His Phe Arg Tyr Phe His Ser Gln Lys
225                 230                 235                 240

ata gca agt gct gta gaa aga tat acg gat gag gtt aga aga gtt tac     949
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ggt gta gtg gag atg gcc ttg gct gaa cgt aga gaa gcg ctg gtg atg      997
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gaa tta gac acg gaa aat gcg gct gca tac tca gct ggt aca aca cca     1045
Glu Leu Asp Thr Glu Asn Ala Ala Ala Tyr Ser Ala Gly Thr Thr Pro
        275                 280                 285

atg tca caa agt cgt ttc ttt gat tat ccc gta tgg ctt gta gga gat     1093
Met Ser Gln Ser Arg Phe Phe Asp Tyr Pro Val Trp Leu Val Gly Asp
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aaa tta act ata gca gat ttg gcc ttt gtc cca tgg aat aat gtc gtg     1141
Lys Leu Thr Ile Ala Asp Leu Ala Phe Val Pro Trp Asn Asn Val Val
305                 310                 315                 320

gat aga att ggc att aat atc aaa att gaa ttt cca gaa gtt tac aaa     1189
Asp Arg Ile Gly Ile Asn Ile Lys Ile Glu Phe Pro Glu Val Tyr Lys
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tgg acg aag cat atg atg aga aga ccc gcg gtc atc aag gca ttg cgt     1237
Trp Thr Lys His Met Met Arg Arg Pro Ala Val Ile Lys Ala Leu Arg
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ggt gga tga aggctgcttt aaaaacaaga aagaaagaag aaggaggaaa             1286
Gly Gly

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Ser Asn Ile Asn Phe Glu Phe Ser Thr Gly Val Asn Asn Asn Asn Asn
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Asn Asn Ser Ser Ser Asn Asn Asn Asn Val Gln Asn Asn Asn Ser Gly
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Arg Asn Gly Ser Gln Asn Asn Asp Asn Glu Asn Asn Ile Lys Asn Thr
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Leu Glu Gln His Arg Gln Gln Gln Gln Ala Phe Ser Asp Met Ser His
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Gly Tyr Thr Leu Phe Ser His Arg Ser Ala Pro Asn Gly Phe Lys Val
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Ala Ile Val Leu Ser Glu Leu Gly Phe His Tyr Asn Thr Ile Phe Leu
    130                 135                 140

Asp Phe Asn Leu Gly Glu His Arg Ala Pro Glu Phe Val Ser Val Asn
145                 150                 155                 160

Pro Asn Ala Arg Val Pro Ala Leu Ile Asp His Gly Met Asp Asn Leu
                165                 170                 175

Ser Ile Trp Glu Ser Gly Ala Ile Leu Leu His Leu Val Asn Lys Tyr
            180                 185                 190

Tyr Lys Glu Thr Gly Asn Pro Leu Leu Trp Ser Asp Asp Leu Ala Asp
        195                 200                 205

Gln Ser Gln Ile Asn Ala Trp Leu Phe Phe Gln Thr Ser Gly His Ala
    210                 215                 220

Pro Met Ile Gly Gln Ala Leu His Phe Arg Tyr Phe His Ser Gln Lys
225                 230                 235                 240

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Gly Val Val Glu Met Ala Leu Ala Glu Arg Arg Glu Ala Leu Val Met
            260                 265                 270

Glu Leu Asp Thr Glu Asn Ala Ala Ala Tyr Ser Ala Gly Thr Thr Pro
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Met Ser Gln Ser Arg Phe Phe Asp Tyr Pro Val Trp Leu Val Gly Asp
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Lys Leu Thr Ile Ala Asp Leu Ala Phe Val Pro Trp Asn Asn Val Val
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Asp Arg Ile Gly Ile Asn Ile Lys Ile Glu Phe Pro Glu Val Tyr Lys
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acttcaccac cctttatttc aggctgatat cttagccttg ttactagtta gaaaaagaca 180

tttttgctgt cagtcactgt caagagattc ttttgctggc atttcttcta gaagcaaaaa 240

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<213> Aequorea victoria

<400> 12
atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60

gatgttaatg gtcacaaatt ttctgtctcc ggtgaaggtg aaggtgatgc tacttacggt 120

aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180

gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240

catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300

aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaaggtga taccttagtt 360

aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420

ttggaataca actataactc tcacaatgtt tacatcatgg ctgacaaaca aaagaatggt 480

atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540

cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600

ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggtcttg 660

ttagaatttg ttactgctgc tggtattacc catggtatgg atgaattgta caaataa 717

<210> 13
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> HA tag-encoding sequence

<400> 13
tacccatacg acgtcccaga ctacgct 27

<210> 14
<211> 645
<212> DNA
<213> Artificial sequence

<220>
<223> Yeast Sup35Rdelta2-5 encoding sequence

<220>
<221> CDS
<222> (1)..(645)

<400> 14
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac 48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1 5 10 15

agc cag aac ggt aac caa caa caa ggt aac aac aga tac caa ggt tat 96
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
20 25 30

caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat 144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
35 40 45

tac caa ggt tat tct ggg tac cca caa ggt ggc cgt gga aat tac aaa 192
Tyr Gln Gly Tyr Ser Gly Tyr Pro Gln Gly Gly Arg Gly Asn Tyr Lys
50 55 60

aac ttc aac tac aat aac aat ttg caa gga tat caa gct ggt ttc caa 240
Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln

```
65                  70                  75                  80

cca cag tct caa ggt atg tct ttg aac gac ttt caa aag caa caa aag      288
Pro Gln Ser Gln Gly Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys
                85                  90                  95

cag gcc gct ccc aaa cca aag aag act ttg aag ctt gtc tcc agt tcc      336
Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser
            100                 105                 110

ggt atc aag ttg gcc aat gct acc aag aag gtt ggc aca aaa cct gcc      384
Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala
        115                 120                 125

gaa tct gat aag aaa gag gaa gag aag tct gct gaa acc aaa gaa cca      432
Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro
    130                 135                 140

act aaa gag cca aca aag gtc gaa gaa cca gtt aaa aag gag gag aaa      480
Thr Lys Glu Pro Thr Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys
145                 150                 155                 160

cca gtc cag act gaa gaa aag acg gag gaa aaa tcg gaa ctt cca aag      528
Pro Val Gln Thr Glu Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys
                165                 170                 175

gta gaa gac ctt aaa atc tct gaa tca aca cat aat acc aac aat gcc      576
Val Glu Asp Leu Lys Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala
            180                 185                 190

aat gtt acc agt gct gat gcc ttg atc aag gaa cag gaa gaa gaa gtg      624
Asn Val Thr Ser Ala Asp Ala Leu Ile Lys Glu Gln Glu Glu Glu Val
        195                 200                 205

gat gac gaa gtt gtt aac gat                                         645
Asp Asp Glu Val Val Asn Asp
    210                 215
```

<210> 15
<211> 215
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Peptide

<400> 15

```
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1               5                   10                  15

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
            20                  25                  30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
        35                  40                  45

Tyr Gln Gly Tyr Ser Gly Tyr Pro Gln Gly Gly Arg Gly Asn Tyr Lys
    50                  55                  60
```

```
Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln
65                  70                  75                  80

Pro Gln Ser Gln Gly Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys
                85                  90                  95

Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser
            100                 105                 110

Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala
        115                 120                 125

Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro
    130                 135                 140

Thr Lys Glu Pro Thr Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys
145                 150                 155                 160

Pro Val Gln Thr Glu Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys
                165                 170                 175

Val Glu Asp Leu Lys Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala
            180                 185                 190

Asn Val Thr Ser Ala Asp Ala Leu Ile Lys Glu Gln Glu Glu Glu Val
        195                 200                 205

Asp Asp Glu Val Val Asn Asp
    210                 215
```

<210> 16
<211> 813
<212> DNA
<213> Artificial sequence

<220>
<223> Yeast Sup35R2E2 encoding sequence

<220>
<221> CDS
<222> (1)..(813)

<400> 16

```
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac       48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1               5                   10                  15

agc cag aac ggt aac caa caa caa ggt aac aac aga tac caa ggt tat       96
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
            20                  25                  30
```

```
caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat      144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
        35                  40                  45

tac caa ggt tat tct ggg tac caa caa ggt ggc tat caa cag tac aat      192
Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
    50                  55                  60

ccc caa ggt ggc tat caa cag tac aat ccc caa ggt ggc tat caa cag      240
Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln
65                  70                  75                  80

tac aat ccc gac gcc ggt tac cag caa cag tat aat cct caa gga ggc      288
Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly
                85                  90                  95

tat caa cag tac aat cct caa ggc ggt tat cag cag caa ttc aat cca      336
Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro
            100                 105                 110

caa ggt ggc cgt gga aat tac aaa aac ttc aac tac aat aac aat ttg      384
Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu
        115                 120                 125

caa gga tat caa gct ggt ttc caa cca cag tct caa ggt atg tct ttg      432
Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu
    130                 135                 140

aac gac ttt caa aag caa caa aag cag gcc gct ccc aaa cca aag aag      480
Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys
145                 150                 155                 160

act ttg aag ctt gtc tcc agt tcc ggt atc aag ttg gcc aat gct acc      528
Thr Leu Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr
                165                 170                 175

aag aag gtt ggc aca aaa cct gcc gaa tct gat aag aaa gag gaa gag      576
Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu
            180                 185                 190

aag tct gct gaa acc aaa gaa cca act aaa gag cca aca aag gtc gaa      624
Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu
        195                 200                 205

gaa cca gtt aaa aag gag gag aaa caa gtc cag act gaa gaa aag acg      672
Glu Pro Val Lys Lys Glu Glu Lys Gln Val Gln Thr Glu Glu Lys Thr
    210                 215                 220

gag gaa aaa tcg gaa ctt cca aag gta gaa gac ctt aaa atc tct gaa      720
Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu
225                 230                 235                 240

tca aca cat aat acc aac aat gcc aat gtt acc agt gct gat gcc ttg      768
Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu
                245                 250                 255

atc aag gaa cag gaa gaa gaa gtg gat gac gaa gtt gtt aac gat          813
Ile Lys Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp
            260                 265                 270
```

<210> 17
<211> 271

<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Peptide

<400> 17

```
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1               5                  10                  15

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
            20                  25                  30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
        35                  40                  45

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
    50                  55                  60

Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln
65                  70                  75                  80

Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly
                85                  90                  95

Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro
            100                 105                 110

Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu
        115                 120                 125

Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu
    130                 135                 140

Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys
145                 150                 155                 160

Thr Leu Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr
                165                 170                 175

Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu
            180                 185                 190

Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu
        195                 200                 205

Glu Pro Val Lys Lys Glu Glu Lys Gln Val Gln Thr Glu Glu Lys Thr
    210                 215                 220
```

```
Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu
225                 230                 235                 240

Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu
                245                 250                 255

Ile Lys Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp
            260                 265                 270
```

<210> 18
<211> 641
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (1)..(633)

<400> 18

```
atg tct aaa aag cgg cca aag cct gga ggg tgg aac acc ggt gga agc        48
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
1               5                   10                  15

cgg tat ccc ggg cag gga agc cct gga ggc aac cgt tac cca cct cag        96
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
            20                  25                  30

ggt ggc acc tgg ggg cag ccc cac ggt ggt ggc tgg gga caa ccc cat       144
Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His
        35                  40                  45

ggg ggc agc tgg gga caa cct cat ggt ggt agt tgg ggt cag ccc cat       192
Gly Gly Ser Trp Gly Gln Pro His Gly Gly Ser Trp Gly Gln Pro His
    50                  55                  60

ggc ggt gga tgg ggc caa gga ggg ggt acc cat aat cag tgg aac aag       240
Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn Lys
65                  70                  75                  80

ccc agc aaa cca aaa acc aac ctc aag cat gtg gca ggg gct gcg gca       288
Pro Ser Lys Pro Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala
                85                  90                  95

gct ggg gca gta gtg ggg ggc ctt ggt ggc tac atg ctg ggg agc gcc       336
Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala
            100                 105                 110

gtg agc agg ccc atg atc cat ttt ggc aac gac tgg gag gac cgc tac       384
Val Ser Arg Pro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr
        115                 120                 125

tac cgt gaa aac atg tac cgc tac cct aac caa gtg tac tac agg cca       432
Tyr Arg Glu Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro
    130                 135                 140

gtg gat cag tac agc aac cag aac aac ttc gtg cac gac tgc ctg aat       480
Val Asp Gln Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Leu Asn
145                 150                 155                 160
```

```
atc acc atc aag cag cac acg gtc acc acc acc acc aag ggg gag aac      528
Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu Asn
                165                 170                 175

ttc acc gag acc gat gtg aag atg atg gag cgc gtg gtg gag cag atg      576
Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met
            180                 185                 190

tgc gtc acc cag tac cag aag gag tcc cag gcc tat tac gac ggg aga      624
Cys Val Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg
        195                 200                 205

aga tcc agc tgataacc                                                641
Arg Ser Ser
    210
```

<210> 19
<211> 211
<212> PRT
<213> Mouse

<400> 19

```
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
1               5                   10                  15

Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
            20                  25                  30

Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His
        35                  40                  45

Gly Gly Ser Trp Gly Gln Pro His Gly Gly Ser Trp Gly Gln Pro His
    50                  55                  60

Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn Lys
65                  70                  75                  80

Pro Ser Lys Pro Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala
                85                  90                  95

Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala
            100                 105                 110

Val Ser Arg Pro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr
        115                 120                 125

Tyr Arg Glu Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro
    130                 135                 140

Val Asp Gln Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Leu Asn
145                 150                 155                 160
```

```
Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu Asn
                165                 170                 175

Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met
            180                 185                 190

Cys Val Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg
        195                 200                 205

Arg Ser Ser
    210
```

<210> 20
<211> 644
<212> DNA
<213> Mesocricetus auratus

<220>
<221> CDS
<222> (1)..(636)

<400> 20

```
atg tct aag aag cgg cca aag cct gga ggg tgg aac act ggc gga agc        48
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
1               5                   10                  15

cga tac cct ggg cag ggc agc cct gga ggc aac cgt tac cca cct cag        96
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
            20                  25                  30

ggt ggc ggc aca tgg ggg caa ccc cat ggt ggt ggc tgg gga cag ccc       144
Gly Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
        35                  40                  45

cat ggt ggt ggc tgg gga cag ccc cat ggt ggt ggc tgg ggt cag ccc       192
His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
    50                  55                  60

cat ggt ggt ggc tgg ggt caa gga ggt ggc acc cac aat cag tgg aac       240
His Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn
65                  70                  75                  80

aag ccc agt aag cca aaa acc aac atg aag cac atg gcc ggc gct gct       288
Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met Ala Gly Ala Ala
                85                  90                  95

gcg gca ggg gcc gtg gtg ggg ggc ctt ggt ggc tac atg ctg ggg agt       336
Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser
            100                 105                 110

gcc atg agc agg ccc atg atg cat ttt ggc aat gac tgg gag gac cgc       384
Ala Met Ser Arg Pro Met Met His Phe Gly Asn Asp Trp Glu Asp Arg
        115                 120                 125

tac tac cgt gaa aac atg aac cgc tac cct aac caa gtg tat tac cgg       432
Tyr Tyr Arg Glu Asn Met Asn Arg Tyr Pro Asn Gln Val Tyr Tyr Arg
    130                 135                 140
```

```
cca gtg gac cag tac aac aac cag aac aac ttt gtg cac gat tgt gtc      480
Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val
145                 150                 155                 160

aac atc acc atc aag cag cac aca gtc acc acc acc acc aag ggg gag      528
Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu
                165                 170                 175

aac ttc acg gag acc gac atc aag ata atg gag gcg gtg gtg gag cag      576
Asn Phe Thr Glu Thr Asp Ile Lys Ile Met Glu Ala Val Val Glu Gln
            180                 185                 190

atg tgt acc acc cag tat cag aag gag tcc cag gcc tac tac gat gga      624
Met Cys Thr Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly
        195                 200                 205

aga agg tcc agc tgataacc                                            644
Arg Arg Ser Ser
    210
```

<210> 21
<211> 212
<212> PRT
<213> Mesocricetus auratus

<400> 21

```
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
1               5                   10                  15

Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
            20                  25                  30

Gly Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
        35                  40                  45

His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
    50                  55                  60

His Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn
65                  70                  75                  80

Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met Ala Gly Ala Ala
                85                  90                  95

Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser
            100                 105                 110

Ala Met Ser Arg Pro Met Met His Phe Gly Asn Asp Trp Glu Asp Arg
        115                 120                 125

Tyr Tyr Arg Glu Asn Met Asn Arg Tyr Pro Asn Gln Val Tyr Tyr Arg
    130                 135                 140
```

```
Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val
145                 150                 155                 160

Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu
                165                 170                 175

Asn Phe Thr Glu Thr Asp Ile Lys Ile Met Glu Ala Val Val Glu Gln
            180                 185                 190

Met Cys Thr Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly
        195                 200                 205

Arg Arg Ser Ser
    210
```

<210> 22
<211> 780
<212> PRT
<213> Saccharomyces cerevisiae

<400> 22

```
Met Lys Lys Lys Asp Asn Ser Asp Asp Lys Asp Asn Val Ala Ser Gly
1               5                   10                  15

Gly Tyr Lys Asn Ala Ala Asp Ala Gly Ser Asn Asn Ala Ser Lys Lys
            20                  25                  30

Ser Ser Tyr Arg Asn Trp Lys Gly Gly Asn Tyr Gly Gly Tyr Ser Tyr
        35                  40                  45

Asn Ser Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr
    50                  55                  60

Asn Asn Tyr Asn Asn Tyr Asn Lys Tyr Asn Gly Gly Tyr Lys Ser Thr
65                  70                  75                  80

Tyr Lys Ser Ala Val Thr Asn Ser Gly Thr Thr Ser Ala Ser Thr Thr
                85                  90                  95

Ser Thr Ser Asn Lys Ser Asn Thr Ser Ser Lys Cys Ser Thr Asp Cys
            100                 105                 110

Lys Asn Lys Gly Lys Gly Asn Ser Thr Gly Lys Trp Lys Val Asp Val
        115                 120                 125

Ser Lys Lys Lys Asn Ser Val Arg Ser Ala Met Ser Asn Ala Ser Gly
    130                 135                 140
```

```
Lys Ala Tyr Asn Val Ala Asp Cys Ser Asp Lys Asn Thr Val Lys Arg
145                 150                 155                 160

Ala Ala His Ala Asp Ser Asn Cys Met Ala Thr Cys Val Thr Asp Tyr
                165                 170                 175

Ser Ser Gly Ala Lys Trp Ala Lys Met Ala Ala Ser Val Val Asp Arg
            180                 185                 190

Arg Asp Ser Ala Asn Asp Thr Lys Asp Ala Val Val Thr Asp Val Ala
        195                 200                 205

Thr Asp Lys Ala Lys Gly Tyr Lys Thr Asp Tyr Val Ser Asp Asn Asp
    210                 215                 220

Ser Arg Tyr Lys Val Asp Thr Asp Ser Lys Val Ser Val Lys Ser Ser
225                 230                 235                 240

Ser Val Thr Cys Ala Cys Thr Ser Ser Val Asn Arg Ser Asn Ser Ser
                245                 250                 255

Ser Ser Arg Thr Val Val Val Asn Thr Arg Val Asn Asn Arg Asn Ser
            260                 265                 270

Gly Lys Val Val Asp Thr Ala Ser Val Arg Ala Lys Ala Asn Val Lys
        275                 280                 285

Asp Asp Ala Asp Lys Asn Lys Ser Gly Arg Thr Gly Arg Asp Asp His
    290                 295                 300

Lys Asp Lys Ala Asp Asp Ser Cys Val Lys Tyr Met Asn Asp Thr Val
305                 310                 315                 320

Lys Tyr Met Ser Leu Thr Val Asp Ser Asn Val Asn Asp Trp Lys Arg
                325                 330                 335

Asp Thr Ala Val Gly Gly Ser Asp Ser Arg Val Lys Asp His Asn Arg
            340                 345                 350

Ala Tyr Lys Arg Ala Asp Asp Gly Val Asn Thr Asp Ser Ala Tyr Gly
        355                 360                 365

Ser Arg Met Asn Lys Thr Asn Arg Lys Gly His Arg Tyr Gly Cys Gly
    370                 375                 380

Arg Asn Gly Ala Gly Lys Ser Thr Met Arg Ala Ala Asn Gly Asp Gly
385                 390                 395                 400
```

```
Asp Lys Asp Thr Arg Thr Cys Val His Lys Gly Gly Asp Asp Val Ser
                405                 410                 415

Ala Asp Ser Thr Ser Arg Ala Ala Ala Ser Val Gly Asp Arg Arg Ala
            420                 425                 430

Thr Val Gly Ser Ser Gly Gly Trp Lys Met Lys Ala Arg Ala Met Lys
        435                 440                 445

Ala Asp Asp Thr Asn His Asp Val Ser Asn Val Lys Trp Tyr His Thr
    450                 455                 460

Asp Thr Ser Val Ser His Asp Ser Gly Asp Thr Val Cys Thr Asp His
465                 470                 475                 480

Tyr Asn Lys Lys Ala Tyr Tyr Lys Gly Asn Ala Ala Val Lys Ala Lys
                485                 490                 495

Ser Tyr Tyr Thr Thr Asp Ser Asn Ala Met Arg Gly Thr Gly Val Lys
            500                 505                 510

Ser Asn Thr Arg Ala Val Ala Lys Met Thr Asp Val Thr Ser Tyr Gly
        515                 520                 525

Ala Lys Ser Ser His Val Ser Cys Ser Ser Ser Ser Arg Val Ala Cys
    530                 535                 540

Gly Asn Gly Ala Gly Lys Ser Thr Leu Thr Gly Val Asn Gly Lys Val
545                 550                 555                 560

Lys His Asn Arg Gly Tyr Ala His Ala His Val Asn His Lys Lys Thr
                565                 570                 575

Ala Asn Tyr Trp Arg Tyr Gly Asp Asp Arg Val Lys Ser Arg Lys Ser
            580                 585                 590

Asp Lys Met Met Thr Lys Asp Asp Asp Gly Arg Gly Lys Arg Ala Ala
        595                 600                 605

Val Gly Arg Lys Lys Lys Ser Tyr Val Lys Trp Lys Tyr Trp Lys Lys
    610                 615                 620

Tyr Asn Ser Trp Val Lys Asp Val Val His Gly Lys Val Lys Asp Asp
625                 630                 635                 640

His Ala Ser Arg Gly Gly Tyr Arg Ser Val Thr Lys His Asp Val Gly
                645                 650                 655
```

```
Asp Ser Ala Asn His Thr Gly Ser Ser Gly Gly Val Lys Val Val Ala
            660                 665                 670

Gly Ala Met Trp Asn Asn His Val Asp Thr Asn Tyr Asp Arg Asp Ser
        675                 680                 685

Gly Ala Ala Val Ala Arg Asp Trp Ser Gly Gly Val Val Met Ser His
    690                 695                 700

Asn Asn Val Gly Ala Cys Trp Val Asn Gly Lys Met Val Lys Gly Ser
705                 710                 715                 720

Ala Val Asp Ser Lys Asp Gly Gly Asn Ala Asp Ala Val Gly Lys Ala
                725                 730                 735

Ser Asn Ala Lys Ser Val Asp Asp Asp Asp Ser Ala Asn Lys Val Lys
            740                 745                 750

Arg Lys Lys Arg Thr Arg Asn Lys Lys Ala Arg Arg Arg Arg Tyr Trp
        755                 760                 765

Ser Ser Lys Gly Thr Lys Val Asp Thr Asp Asp Asp
    770                 775                 780
```

<210> 23
<211> 1075
<212> PRT
<213> Saccharomyces cerevisiae

<400> 23

```
Met Asp Asn Lys Arg Leu Tyr Asn Gly Asn Leu Ser Asn Ile Pro Glu
1               5                   10                  15

Val Ile Asp Pro Gly Ile Thr Ile Pro Ile Tyr Glu Glu Asp Ile Arg
            20                  25                  30

Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val Ser Asp
        35                  40                  45

Lys Arg Gly Arg Ser Ser Ser Thr Ser Pro Gln Lys Ile Gly Ser Tyr
    50                  55                  60

Arg Thr Arg Ala Gly Arg Phe Ser Asp Thr Lys Thr Asn Lys Lys Pro
65                  70                  75                  80

Ser Ile Ser Ala Lys Leu His His Ser Lys Lys Ser Thr Pro Val Val
                85                  90                  95
```

```
Val Val Pro Pro Thr Ser Ser Thr Pro Asp Ser Lys Asn Ser Thr Thr
            100                 105                 110

Tyr Ala Pro Arg Val Ser Ser Asp Ser Phe Thr Val Ala Thr Pro Leu
        115                 120                 125

Ser Leu Gln Ser Thr Thr Thr Arg Thr Arg Thr Arg Asn Asn Thr Val
    130                 135                 140

Ser Ser Gln Ile Thr Ala Ser Ser Ser Lys Thr Thr Asp Val Gly Asn
145                 150                 155                 160

Ala Thr Ser Ala Asn Ile Trp Ser Ala Asn Ala Glu Ser Asn Thr Ser
                165                 170                 175

Ser Ser Pro Leu Phe Asp Tyr Pro Leu Ala Thr Ser Tyr Phe Glu Pro
            180                 185                 190

Leu Thr Arg Phe Lys Ser Thr Asp Asn Tyr Thr Leu Pro Gln Thr Ala
        195                 200                 205

Gln Leu Asn Ser Phe Leu Glu Lys Asn Gly Asn Pro Asn Ile Trp Ser
    210                 215                 220

Ser Ala Gly Asn Ser Asn Thr Asp His Leu Asn Thr Pro Ile Val Asn
225                 230                 235                 240

Arg Gln Arg Ser Gln Ser Gln Asn Thr Thr Asn Arg Val Tyr Thr Asp
                245                 250                 255

Ala Pro Tyr Tyr Gln Gln Pro Ala Gln Asn Tyr Gln Val Tyr Val Pro
            260                 265                 270

Pro Arg Val Pro Lys Ser Thr Ser Ile Ser Pro Val Ile Leu Asp Asp
        275                 280                 285

Val Asp Pro Ala Ser Ile Asn Trp Ile Thr Ala Asn Gln Lys Val Pro
    290                 295                 300

Leu Val Asn Gln Ile Ser Ala Leu Leu Pro Thr Asn Thr Ile Ser Ile
305                 310                 315                 320

Ser Asn Val Phe Pro Leu Gln Pro Thr Gln Gln His Gln Gln Asn Ala
                325                 330                 335

Val Asn Leu Thr Ser Thr Ser Leu Ala Thr Leu Cys Ser Gln Tyr Gly
            340                 345                 350
```

Lys Val Leu Ser Ala Arg Thr Leu Arg Gly Leu Asn Met Ala Leu Val
355 360 365

Glu Phe Ser Thr Val Glu Ser Ala Ile Cys Ala Leu Glu Ala Leu Gln
370 375 380

Gly Lys Glu Leu Ser Lys Val Gly Ala Pro Ser Thr Val Ser Phe Ala
385 390 395 400

Arg Val Leu Pro Met Tyr Glu Gln Pro Leu Asn Val Asn Gly Phe Asn
405 410 415

Asn Thr Pro Lys Gln Pro Leu Leu Gln Glu Gln Leu Asn His Gly Val
420 425 430

Leu Asn Tyr Gln Lys Gln Gln Ser Leu Gln Gln Pro Glu Leu Gln Gln
435 440 445

Gln Pro Thr Ser Phe Asn Gln Pro Asn Leu Thr Tyr Cys Asn Pro Thr
450 455 460

Gln Asn Leu Ser His Leu Gln Leu Ser Ser Asn Glu Asn Glu Pro Tyr
465 470 475 480

Pro Phe Pro Leu Pro Pro Pro Ser Leu Ser Asp Ser Lys Lys Asp Ile
485 490 495

Leu His Thr Ile Ser Ser Phe Lys Leu Glu Tyr Asp His Leu Glu Leu
500 505 510

Asn His Leu Leu Gln Asn Ala Leu Lys Asn Lys Gly Val Ser Asp Thr
515 520 525

Asn Tyr Phe Gly Pro Leu Pro Glu His Asn Ser Lys Val Pro Lys Arg
530 535 540

Lys Asp Thr Phe Asp Ala Pro Lys Leu Arg Glu Leu Arg Lys Gln Phe
545 550 555 560

Asp Ser Asp Ser Leu Ser Thr Ile Glu Met Glu Gln Leu Ala Ile Val
565 570 575

Met Leu Asp Gln Leu Pro Glu Leu Ser Ser Asp Tyr Leu Gly Asn Thr
580 585 590

Val Ile Gln Lys Leu Phe Glu Asn Ser Ser Asn Ile Ile Arg Asp Ile
595 600 605

Met Leu Arg Lys Cys Asn Lys Tyr Leu Thr Ser Met Gly Val His Lys
610 615 620

Asn Gly Thr Trp Val Cys Gln Lys Ile Ile Lys Met Ala Asn Thr Pro
625 630 635 640

Arg Gln Ile Asn Leu Val Thr Ser Gly Val Ser Asp Tyr Cys Thr Pro
645 650 655

Leu Phe Asn Asp Gln Phe Gly Asn Tyr Val Ile Gln Gly Ile Leu Lys
660 665 670

Phe Gly Phe Pro Trp Asn Ser Phe Ile Phe Glu Ser Val Leu Ser His
675 680 685

Phe Trp Thr Ile Val Gln Asn Arg Tyr Gly Ser Arg Ala Val Arg Ala
690 695 700

Cys Leu Glu Ala Asp Ser Ile Ile Thr Gln Cys Gln Leu Leu Thr Ile
705 710 715 720

Thr Ser Leu Ile Ile Val Leu Ser Pro Tyr Leu Ala Thr Asp Thr Asn
725 730 735

Gly Thr Leu Leu Ile Thr Trp Leu Leu Asp Thr Cys Thr Leu Pro Asn
740 745 750

Lys Asn Leu Ile Leu Cys Asp Lys Leu Val Asn Lys Asn Leu Val Lys
755 760 765

Leu Cys Cys His Lys Leu Gly Ser Leu Thr Val Leu Lys Ile Leu Asn
770 775 780

Leu Arg Gly Gly Glu Glu Glu Ala Leu Ser Lys Asn Lys Ile Ile His
785 790 795 800

Ala Ile Phe Asp Gly Pro Ile Ser Ser Asp Ser Ile Leu Phe Gln Ile
805 810 815

Leu Asp Glu Gly Asn Tyr Gly Pro Thr Phe Ile Tyr Lys Val Leu Thr
820 825 830

Ser Arg Ile Leu Asp Asn Ser Val Arg Asp Glu Ala Ile Thr Lys Ile
835 840 845

Arg Gln Leu Ile Leu Asn Ser Asn Ile Asn Leu Gln Ser Arg Gln Leu
850 855 860

```
Leu Glu Glu Val Gly Lys Ser Ser Ala Gly Ile Ser Pro Lys Gln Ser
865                 870                 875                 880

Ser Lys Asn His Arg Lys Gln His Pro Gln Gly Phe His Ser Pro Gly
                885                 890                 895

Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser Ser Asn Ser Arg
            900                 905                 910

His Asn Ser Val Ile Gln Met Asn Asn Ala Gly Pro Thr Pro Ala Leu
        915                 920                 925

Asn Phe Asn Pro Ala Pro Met Ser Glu Ile Asn Ser Tyr Phe Asn Asn
    930                 935                 940

Gln Gln Val Val Tyr Ser Gly Asn Gln Asn Gln Asn Gln Asn Gly Asn
945                 950                 955                 960

Ser Asn Gly Leu Asp Glu Leu Asn Ser Gln Phe Asp Ser Phe Arg Ile
                965                 970                 975

Ala Asn Gly Thr Asn Leu Ser Leu Pro Ile Val Asn Leu Pro Asn Val
            980                 985                 990

Ser Asn Asn Asn Asn Asn Tyr Asn  Asn Ser Gly Tyr Ser  Ser Gln Met
        995                 1000                1005

Asn Pro  Leu Ser Arg Ser Val  Ser His Asn Asn Asn  Asn Asn Thr
    1010                1015                1020

Asn Asn  Tyr Asn Asn Asn Asp  Asn Asp Asn Asn Asn  Asn Asn Asn
    1025                1030                1035

Asn Asn  Asn Asn Asn Asn Asn  Asn Asn Asn Asn Asn  Asn Asn Asn
    1040                1045                1050

Ser Asn  Asn Ser Asn Asn Asn  Asn Asn Asn Asp Thr  Ser Leu Tyr
    1055                1060                1065

Arg Tyr  Arg Ser Tyr Gly Tyr
    1070                1075
```

<210> 24
<211> 76
<212> PRT
<213> Saccharomyces cerevisiae

<400> 24

```
Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Lys Ser Tyr Ser
1               5                  10                  15

Arg Ser Asn Ser Ser Ala His Asn Lys Thr Arg Gly Tyr Tyr Tyr His
            20                  25                  30

Gly Tyr Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn
        35                  40                  45

Gly Tyr Asn Gly Tyr Asn Gly His Val Tyr Val Arg Gly Asn Gly Cys
    50                  55                  60

Ala Ala Cys Ala Ala Cys Cys Cys Thr Met Asp Met
65                  70                  75
```

<210> 25
<211> 380
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25

```
Met Ser Ser Asp Asp Asn Asp Tyr Gly Asp Asp Lys Thr Thr Thr Val
1               5                  10                  15

Lys Lys Asn Lys Ala Gly Ser Gly Thr Ser Asp Ala Ala Ala Ser Ser
            20                  25                  30

Ser Asn Lys Asn Asn Asn Ser Asn Asn Ser Ser Ser Asn Asn Ser Asn
        35                  40                  45

Asp Thr Ser Ser Ser Lys Asp Gly Thr Ala Asn Asp Lys Gly Ser Asn
    50                  55                  60

Asp Thr Lys Asn Lys Lys Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn
65                  70                  75                  80

Ala Ser Ser Ala Gly Ser Gly Trp Thr Met Ser Ser Ser Ser Val Thr
                85                  90                  95

Thr Lys Arg Ser Lys Ala Asp Ser Lys Ser Cys Lys Asn Gly Gly Asn
            100                 105                 110

Trp Asp Thr Thr Asp Asn Arg Tyr Gly Lys Tyr Gly Thr Val Thr Asp
        115                 120                 125

Lys Met Lys Asp Ala Thr Gly Arg Ser Arg Gly Gly Ser Lys Ser Ser
    130                 135                 140
```

```
Val Asp Val Val Lys Thr His Asp Gly Lys Val Asp Lys Arg Ala Arg
145                 150                 155                 160

Asp Asp Lys Thr Gly Lys Val Gly Gly Gly Asp Val Arg Lys Ser Trp
                165                 170                 175

Gly Thr Asp Ala Met Asp Lys Asp Thr Gly Ser Arg Gly Gly Val Thr
            180                 185                 190

Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Asn Lys Asp Lys Asp
        195                 200                 205

Arg Lys Lys Arg Ala Arg His Met Lys Ser Ser Asn Asn Gly Gly Asn
    210                 215                 220

Asn Gly Gly Asn Asn Met Asn Arg Arg Gly Gly Asn Gly Asn Gly Asp
225                 230                 235                 240

Asn Met Tyr Asn Met Met Gly Gly Tyr Asn Met Met Asn Ala Met Thr
                245                 250                 255

Asp Tyr Tyr Lys Met Tyr Tyr Met Lys Thr Gly Met Asp Tyr Thr Met
            260                 265                 270

Tyr Met Met Ala Met Met Met Gly Ala Met Asn Ala Met Thr Asn Asp
        275                 280                 285

Ser Asn Ala Thr Gly Ser Ala Ser Asp Ser Asp Asn Asn Lys Ser Asn
    290                 295                 300

Asp Val Thr Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Asn Asn Gly
305                 310                 315                 320

Lys Gly Ser Tyr Asn Asp Asp His Asn Ser Gly Tyr Gly Tyr Asn Arg
                325                 330                 335

Asp Arg Gly Asp Arg Asp Arg Asn Asp Arg Asp Arg Asp Tyr Asn His
            340                 345                 350

Arg Ser Gly Gly Asn His Arg Arg Asn Gly Arg Gly Gly Arg Gly Gly
        355                 360                 365

Tyr Asn Arg Arg Asn Asn Gly Tyr His Tyr Asn Arg
    370                 375                 380
```

<210> 26
<211> 256
<212> PRT

<213> Saccharomyces cerevisiae

<400> 26

```
Met Ser Ala Thr His Val Ser Val Val Asp Ala Val His Ala Asp Ala
1               5                  10                  15

Val Ser Ala Ser Ala Ala Asn Asp Val Ser Asn Ala Tyr Gly Ser His
            20                  25                  30

Ser Val Asp Tyr Ala His His His Tyr Tyr Gly His Met His Gly Arg
        35                  40                  45

Met His His Arg Gly Ser Asn Thr Arg Val Arg Asp Val Ser Asn Gly
    50                  55                  60

Gly Met Lys Val Lys Asn Gly Ala Val Ala Ser Ala Ala Lys Ala Val
65                  70                  75                  80

His Gly Lys Ser Ala Asn Val Val Tyr Ser Lys Ala Lys Arg Tyr Arg
                85                  90                  95

Thr Met Lys Asn Gly Cys Ser Trp Asp Lys Asp Ala Arg Asn Ser Thr
            100                 105                 110

Thr Ser Ser Val Asn Thr Arg Asp Asp Gly Thr Gly Ala Ser Val Ala
        115                 120                 125

Arg Asn Asn Arg Gly Ser Val Thr Val Arg Asp Asp Asn Arg Arg Ser
    130                 135                 140

Asn Arg Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg
145                 150                 155                 160

Gly Gly Ser Arg Gly Gly Gly Gly Arg Gly Gly Gly Gly Arg Gly Gly
                165                 170                 175

Tyr Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Tyr Ser Arg Gly Gly
            180                 185                 190

Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Ser Asp Gly Gly Tyr Asp Ser
        195                 200                 205

Arg Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Arg Asn Asp Tyr Gly
    210                 215                 220

Arg Gly Ser Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Gly Arg Gly Asp
225                 230                 235                 240
```

Tyr Gly Arg Asp Ala Tyr Arg Thr Arg Asp Ala Arg Arg Ser Thr Arg
245 250 255

<210> 27
<211> 286
<212> PRT
<213> Saccharomyces cerevisiae

<400> 27

Met Ser Asp Ile Glu Glu Gly Thr Pro Thr Asn Asn Gly Gln Gln Lys
1 5 10 15

Glu Arg Arg Lys Ile Glu Ile Lys Phe Ile Glu Asn Lys Thr Arg Arg
20 25 30

His Val Thr Phe Ser Lys Arg Lys His Gly Ile Met Lys Lys Ala Phe
35 40 45

Glu Leu Ser Val Leu Thr Gly Thr Gln Val Leu Leu Leu Val Val Ser
50 55 60

Glu Thr Gly Leu Val Tyr Thr Phe Ser Thr Pro Lys Phe Glu Pro Ile
65 70 75 80

Val Thr Gln Gln Glu Gly Arg Asn Lys Ile Gln Ala Cys Leu Asn Ala
85 90 95

Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Asp Gly Asp Asp Asp Asp
100 105 110

Asp Asp Asp Asp Asp Gly Asn Asp Met Gln Arg Gln Gln Pro Gln Gln
115 120 125

Gln Gln Pro Gln Gln Gln Gln Gln Val Leu Asn Ala His Ala Asn Ser
130 135 140

Leu Gly His Leu Asn Gln Asp Gln Val Pro Ala Gly Ala Leu Lys Gln
145 150 155 160

Glu Val Lys Ser Gln Leu Leu Gly Gly Ala Asn Pro Asn Gln Asn Ser
165 170 175

Met Ile Gln Gln Gln Gln His His Thr Gln Asn Ser Gln Pro Gln Gln
180 185 190

Gln Gln Gln Gln Gln Pro Gln Gln Gln Met Ser Gln Gln Gln Met Ser
195 200 205

```
Gln His Pro Arg Pro Gln Gln Gly Ile Pro His Pro Gln Gln Ser Gln
    210                 215                 220

Pro Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln
225                 230                 235                 240

Gln Gln Gln Gln Gln Pro Leu Thr Gly Ile His Gln Pro His Gln Gln
                245                 250                 255

Ala Phe Ala Asn Ala Ala Ser Pro Tyr Leu Asn Ala Glu Gln Asn Ala
            260                 265                 270

Ala Tyr Gln Gln Tyr Phe Gln Glu Pro Gln Gln Gly Gln Tyr
        275                 280                 285
```

<210> 28
<211> 414
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28

```
Met Ala Lys Thr Thr Lys Val Lys Gly Asn Lys Lys Glu Val Lys Ala
1               5                   10                  15

Ser Lys Gln Ala Lys Glu Glu Lys Ala Lys Ala Val Ser Ser Ser Ser
            20                  25                  30

Ser Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Glu Ser Glu
        35                  40                  45

Ser Glu Ser Glu Ser Glu Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser
    50                  55                  60

Glu Ser Ser Ser Ser Ser Ser Ser Asp Ser Glu Ser Glu Ala Glu Thr
65                  70                  75                  80

Lys Lys Glu Glu Ser Lys Asp Ser Ser Ser Ser Ser Ser Asp Ser Ser
                85                  90                  95

Ser Asp Glu Glu Glu Glu Glu Glu Lys Glu Glu Thr Lys Lys Glu Glu
            100                 105                 110

Ser Lys Glu Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser Asp
        115                 120                 125

Ser Glu Ser Glu Lys Glu Glu Ser Asn Asp Lys Lys Arg Lys Ser Glu
    130                 135                 140
```

```
Asp Ala Glu Glu Glu Glu Asp Glu Glu Ser Ser Asn Lys Lys Gln Lys
145                 150                 155                 160

Asn Glu Glu Thr Glu Glu Pro Ala Thr Ile Phe Val Gly Arg Leu Ser
                165                 170                 175

Trp Ser Ile Asp Asp Glu Trp Leu Lys Lys Glu Phe Glu His Ile Gly
            180                 185                 190

Gly Val Ile Gly Ala Arg Val Ile Tyr Glu Arg Gly Thr Asp Arg Ser
        195                 200                 205

Arg Gly Tyr Gly Tyr Val Asp Phe Glu Asn Lys Ser Tyr Ala Glu Lys
    210                 215                 220

Ala Ile Gln Glu Met Gln Gly Lys Glu Ile Asp Gly Arg Pro Ile Asn
225                 230                 235                 240

Cys Asp Met Ser Thr Ser Lys Pro Ala Gly Asn Asn Asp Arg Ala Lys
                245                 250                 255

Lys Phe Gly Asp Thr Pro Ser Glu Pro Ser Asp Thr Leu Phe Leu Gly
            260                 265                 270

Asn Leu Ser Phe Asn Ala Asp Arg Asp Ala Ile Phe Glu Leu Phe Ala
        275                 280                 285

Lys His Gly Glu Val Val Ser Val Arg Ile Pro Thr His Pro Glu Thr
    290                 295                 300

Glu Gln Pro Lys Gly Phe Gly Tyr Val Gln Phe Ser Asn Met Glu Asp
305                 310                 315                 320

Ala Lys Lys Ala Leu Asp Ala Leu Gln Gly Glu Tyr Ile Asp Asn Arg
                325                 330                 335

Pro Val Arg Leu Asp Phe Ser Ser Pro Arg Pro Asn Asn Asp Gly Gly
            340                 345                 350

Arg Gly Gly Ser Arg Gly Phe Gly Gly Arg Gly Gly Gly Arg Gly Gly
        355                 360                 365

Asn Arg Gly Phe Gly Gly Arg Gly Gly Ala Arg Gly Gly Arg Gly Gly
    370                 375                 380

Phe Arg Pro Ser Gly Ser Gly Ala Asn Thr Ala Pro Leu Gly Arg Ser
385                 390                 395                 400
```

```
Arg Asn Thr Ala Ser Phe Ala Gly Ser Lys Lys Thr Phe Asp
                405                 410
```

<210> 29
<211> 405
<212> PRT
<213> Saccharomyces cerevisiae

<400> 29

```
Met Asp Thr Asp Lys Leu Ile Ser Glu Ala Glu Ser His Phe Ser Gln
1               5                   10                  15

Gly Asn His Ala Glu Ala Val Ala Lys Leu Thr Ser Ala Ala Gln Ser
            20                  25                  30

Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
        35                  40                  45

Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
    50                  55                  60

Gln Asp Arg Ala Ala Gly Gly Gly Ser Ser Phe Met Asn Thr Leu Met
65                  70                  75                  80

Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
                85                  90                  95

Leu Ala Thr Val Met Thr His Ser Ser Asn Lys Gly Ser Ser Asn Arg
            100                 105                 110

Gly Phe Asp Val Gly Thr Cys Met Ser Met Leu Ser Gly Ser Gly Gly
        115                 120                 125

Gly Ser Gln Ser Met Gly Ala Ser Gly Leu Ala Ala Leu Ala Ser Gln
    130                 135                 140

Phe Phe Lys Ser Gly Asn Asn Ser Gln Gly Gln Gly Gln Gly Gln Gly
145                 150                 155                 160

Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Ser Phe Thr Ala
                165                 170                 175

Leu Ala Ser Leu Ala Ser Ser Phe Met Asn Ser Asn Asn Asn Asn Gln
            180                 185                 190

Gln Gly Gln Asn Gln Ser Ser Gly Gly Ser Ser Phe Gly Ala Leu Ala
        195                 200                 205
```

```
Ser Met Ala Ser Ser Phe Met His Ser Asn Asn Asn Gln Asn Ser Asn
    210                 215                 220

Asn Ser Gln Gln Gly Tyr Asn Gln Ser Tyr Gln Asn Gly Asn Gln Asn
225                 230                 235                 240

Ser Gln Gly Tyr Asn Asn Gln Gln Tyr Gln Gly Gly Asn Gly Gly Tyr
                245                 250                 255

Gln Gln Gln Gln Gly Gln Ser Gly Gly Ala Phe Ser Ser Leu Ala Ser
            260                 265                 270

Met Ala Gln Ser Tyr Leu Gly Gly Gly Gln Thr Gln Ser Asn Gln Gln
        275                 280                 285

Gln Tyr Asn Gln Gln Gly Gln Asn Asn Gln Gln Gln Tyr Gln Gln Gln
    290                 295                 300

Gly Gln Asn Tyr Gln His Gln Gln Gln Gly Gln Gln Gln Gln Gln Gly
305                 310                 315                 320

His Ser Ser Ser Phe Ser Ala Leu Ala Ser Met Ala Ser Ser Tyr Leu
                325                 330                 335

Gly Asn Asn Ser Asn Ser Asn Ser Ser Tyr Gly Gly Gln Gln Gln Ala
            340                 345                 350

Asn Glu Tyr Gly Arg Pro Gln His Asn Gly Gln Gln Gln Ser Asn Glu
        355                 360                 365

Tyr Gly Arg Pro Gln Tyr Gly Gly Asn Gln Asn Ser Asn Gly Gln His
    370                 375                 380

Glu Ser Phe Asn Phe Ser Gly Asn Phe Ser Gln Gln Asn Asn Asn Gly
385                 390                 395                 400

Asn Gln Asn Arg Tyr
```

<210> 30
<211> 964
<212> PRT
<213> Saccharomyces cerevisiae

<400> 30

```
Met Pro Glu Gln Ala Gln Gln Gly Glu Gln Ser Val Lys Arg Arg Arg
1               5                   10                  15
```

```
Val Thr Arg Ala Cys Asp Glu Cys Arg Lys Lys Lys Val Lys Cys Asp
            20                  25                  30

Gly Gln Gln Pro Cys Ile His Cys Thr Val Tyr Ser Tyr Glu Cys Thr
        35                  40                  45

Tyr Lys Lys Pro Thr Lys Arg Thr Gln Asn Ser Gly Asn Ser Gly Val
    50                  55                  60

Leu Thr Leu Gly Asn Val Thr Thr Gly Pro Ser Ser Ser Thr Val Val
65                  70                  75                  80

Ala Ala Ala Ala Ser Asn Pro Asn Lys Leu Leu Ser Asn Ile Lys Thr
                85                  90                  95

Glu Arg Ala Ile Leu Pro Gly Ala Ser Thr Ile Pro Ala Ser Asn Asn
            100                 105                 110

Pro Ser Lys Pro Arg Lys Tyr Lys Thr Lys Ser Thr Arg Leu Gln Ser
        115                 120                 125

Lys Ile Asp Arg Tyr Lys Gln Ile Phe Asp Glu Val Phe Pro Gln Leu
    130                 135                 140

Pro Asp Ile Asp Asn Leu Asp Ile Pro Val Phe Leu Gln Ile Phe His
145                 150                 155                 160

Asn Phe Lys Arg Asp Ser Gln Ser Phe Leu Asp Asp Thr Val Lys Glu
                165                 170                 175

Tyr Thr Leu Ile Val Asn Asp Ser Ser Ser Pro Ile Gln Pro Val Leu
            180                 185                 190

Ser Ser Asn Ser Lys Asn Ser Thr Pro Asp Glu Phe Leu Pro Asn Met
        195                 200                 205

Lys Ser Asp Ser Asn Ser Ala Ser Ser Asn Arg Glu Gln Asp Ser Val
    210                 215                 220

Asp Thr Tyr Ser Asn Ile Pro Val Gly Arg Glu Ile Lys Ile Ile Leu
225                 230                 235                 240

Pro Pro Lys Ala Ile Ala Leu Gln Phe Val Lys Ser Thr Trp Glu His
                245                 250                 255

Cys Cys Val Leu Leu Arg Phe Tyr His Arg Pro Ser Phe Ile Arg Gln
            260                 265                 270
```

```
Leu Asp Glu Leu Tyr Glu Thr Asp Pro Asn Asn Tyr Thr Ser Lys Gln
        275                 280                 285

Met Gln Phe Leu Pro Leu Cys Tyr Ala Ala Ile Ala Val Gly Ala Leu
    290                 295                 300

Phe Ser Lys Ser Ile Val Ser Asn Asp Ser Ser Arg Glu Lys Phe Leu
305                 310                 315                 320

Gln Asp Glu Gly Tyr Lys Tyr Phe Ile Ala Ala Arg Lys Leu Ile Asp
                325                 330                 335

Ile Thr Asn Ala Arg Asp Leu Asn Ser Ile Gln Ala Ile Leu Met Leu
            340                 345                 350

Ile Ile Phe Leu Gln Cys Ser Ala Arg Leu Ser Thr Cys Tyr Thr Tyr
        355                 360                 365

Ile Gly Val Ala Met Arg Ser Ala Leu Arg Ala Gly Phe His Arg Lys
    370                 375                 380

Leu Ser Pro Asn Ser Gly Phe Ser Pro Ile Glu Ile Glu Met Arg Lys
385                 390                 395                 400

Arg Leu Phe Tyr Thr Ile Tyr Lys Leu Asp Val Tyr Ile Asn Ala Met
                405                 410                 415

Leu Gly Leu Pro Arg Ser Ile Ser Pro Asp Asp Phe Asp Gln Thr Leu
            420                 425                 430

Pro Leu Asp Leu Ser Asp Glu Asn Ile Thr Glu Val Ala Tyr Leu Pro
        435                 440                 445

Glu Asn Gln His Ser Val Leu Ser Ser Thr Gly Ile Ser Asn Glu His
    450                 455                 460

Thr Lys Leu Phe Leu Ile Leu Asn Glu Ile Ile Ser Glu Leu Tyr Pro
465                 470                 475                 480

Ile Lys Lys Thr Ser Asn Ile Ile Ser His Glu Thr Val Thr Ser Leu
                485                 490                 495

Glu Leu Lys Leu Arg Asn Trp Leu Asp Ser Leu Pro Lys Glu Leu Ile
            500                 505                 510

Pro Asn Ala Glu Asn Ile Asp Pro Glu Tyr Glu Arg Ala Asn Arg Leu
        515                 520                 525
```

```
Leu His Leu Ser Phe Leu His Val Gln Ile Ile Leu Tyr Arg Pro Phe
    530                 535                 540

Ile His Tyr Leu Ser Arg Asn Met Asn Ala Glu Asn Val Asp Pro Leu
545                 550                 555                 560

Cys Tyr Arg Arg Ala Arg Asn Ser Ile Ala Val Ala Arg Thr Val Ile
                565                 570                 575

Lys Leu Ala Lys Glu Met Val Ser Asn Asn Leu Leu Thr Gly Ser Tyr
            580                 585                 590

Trp Tyr Ala Cys Tyr Thr Ile Phe Tyr Ser Val Ala Gly Leu Leu Phe
        595                 600                 605

Tyr Ile His Glu Ala Gln Leu Pro Asp Lys Asp Ser Ala Arg Glu Tyr
    610                 615                 620

Tyr Asp Ile Leu Lys Asp Ala Glu Thr Gly Arg Ser Val Leu Ile Gln
625                 630                 635                 640

Leu Lys Asp Ser Ser Met Ala Ala Ser Arg Thr Tyr Asn Leu Leu Asn
                645                 650                 655

Gln Ile Phe Glu Lys Leu Asn Ser Lys Thr Ile Gln Leu Thr Ala Leu
            660                 665                 670

His Ser Ser Pro Ser Asn Glu Ser Ala Phe Leu Val Thr Asn Asn Ser
        675                 680                 685

Ser Ala Leu Lys Pro His Leu Gly Asp Ser Leu Gln Pro Pro Val Phe
    690                 695                 700

Phe Ser Ser Gln Asp Thr Lys Asn Ser Phe Ser Leu Ala Lys Ser Glu
705                 710                 715                 720

Glu Ser Thr Asn Asp Tyr Ala Met Ala Asn Tyr Leu Asn Asn Thr Pro
                725                 730                 735

Ile Ser Glu Asn Pro Leu Asn Glu Ala Gln Gln Gln Asp Gln Val Ser
            740                 745                 750

Gln Gly Thr Thr Asn Met Ser Asn Glu Arg Asp Pro Asn Asn Phe Leu
        755                 760                 765

Ser Ile Asp Ile Arg Leu Asp Asn Asn Gly Gln Ser Asn Ile Leu Asp
    770                 775                 780
```

```
Ala Thr Asp Asp Val Phe Ile Arg Asn Asp Gly Asp Ile Pro Thr Asn
785                 790                 795                 800

Ser Ala Phe Asp Phe Ser Ser Ser Lys Ser Asn Ala Ser Asn Asn Ser
                805                 810                 815

Asn Pro Asp Thr Ile Asn Asn Asn Tyr Asn Asn Val Ser Gly Lys Asn
            820                 825                 830

Asn Asn Asn Asn Asn Ile Thr Asn Asn Ser Asn Asn Asn His Asn Asn
        835                 840                 845

Asn Asn Asn Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
    850                 855                 860

Asn Asn Asn Asn Asn Ser Gly Asn Ser Ser Asn Asn Asn Asn Asn Asn
865                 870                 875                 880

Asn Asn Asn Lys Asn Asn Asn Asp Phe Gly Ile Lys Ile Asp Asn Asn
                885                 890                 895

Ser Pro Ser Tyr Glu Gly Phe Pro Gln Leu Gln Ile Pro Leu Ser Gln
            900                 905                 910

Asp Asn Leu Asn Ile Glu Asp Lys Glu Glu Met Ser Pro Asn Ile Glu
        915                 920                 925

Ile Lys Asn Glu Gln Asn Met Thr Asp Ser Asn Asp Ile Leu Gly Val
    930                 935                 940

Phe Asp Gln Leu Asp Ala Gln Leu Phe Gly Lys Tyr Leu Pro Leu Asn
945                 950                 955                 960

Tyr Pro Ser Glu
```

<210> 31
<211> 758
<212> PRT
<213> Saccharomyces cerevisiae

<400> 31

```
Met Asp Asn Thr Thr Asn Ile Asn Thr Asn Glu Arg Ser Ser Asn Thr
1               5                   10                  15

Asp Phe Ser Ser Ala Pro Asn Ile Lys Gly Leu Asn Ser His Thr Gln
            20                  25                  30
```

```
Leu Asn Phe Asp Ala Asp Ser Arg Val Phe Val Ser Asp Val Met Ala
        35                  40                  45

Lys Asn Ser Lys Gln Leu Leu Tyr Ala His Ile Tyr Asn Tyr Leu Ile
    50                  55                  60

Lys Asn Asn Tyr Trp Asn Ser Ala Ala Lys Phe Leu Ser Glu Ala Asp
65                  70                  75                  80

Leu Pro Leu Ser Arg Ile Asn Gly Ser Ala Ser Gly Gly Lys Thr Ser
                85                  90                  95

Lys Asn Ala Ser Leu Lys Gln Gly Leu Met Asp Ile Ala Ser Lys Gly
            100                 105                 110

Asp Ile Val Ser Glu Asp Gly Leu Leu Pro Ser Lys Met Leu Met Asp
        115                 120                 125

Ala Asn Asp Thr Phe Leu Leu Glu Trp Trp Glu Ile Phe Gln Ser Leu
    130                 135                 140

Phe Asn Gly Asp Leu Glu Ser Gly Tyr Gln Gln Asp His Asn Pro Leu
145                 150                 155                 160

Arg Glu Arg Ile Ile Pro Ile Leu Pro Ala Asn Ser Lys Ser Asn Met
                165                 170                 175

Pro Ser His Phe Ser Asn Leu Pro Pro Asn Val Ile Pro Pro Thr Gln
            180                 185                 190

Asn Ser Phe Pro Val Ser Glu Glu Ser Phe Arg Pro Asn Gly Asp Gly
        195                 200                 205

Ser Asn Phe Asn Leu Asn Asp Pro Thr Asn Arg Asn Val Ser Glu Arg
    210                 215                 220

Phe Leu Ser Arg Thr Ser Gly Val Tyr Asp Lys Gln Asn Ser Ala Asn
225                 230                 235                 240

Phe Ala Pro Asp Thr Ala Ile Asn Ser Asp Ile Ala Gly Asn Asn Tyr
                245                 250                 255

Ala Thr Ile Asn Leu His Lys His Phe Asn Asp Leu Gln Ser Pro Ala
            260                 265                 270

Gln Pro Gln Gln Ser Ser Gln Gln Gln Ile Gln Gln Pro Gln His Gln
        275                 280                 285
```

```
Pro Gln His Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
    290                 295                 300

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
305                 310                 315                 320

Gln Gln Gln His Gln Gln Gln Gln Gln Thr Pro Tyr Pro Ile Val Asn
                325                 330                 335

Pro Gln Met Val Pro His Ile Pro Ser Glu Asn Ser His Ser Thr Gly
            340                 345                 350

Leu Met Pro Ser Val Pro Pro Thr Asn Gln Gln Phe Asn Ala Gln Thr
        355                 360                 365

Gln Ser Ser Met Phe Ser Asp Gln Gln Arg Phe Phe Gln Tyr Gln Leu
    370                 375                 380

His His Gln Asn Gln Gly Gln Ala Pro Ser Phe Gln Gln Ser Gln Ser
385                 390                 395                 400

Gly Arg Phe Asp Asp Met Asn Ala Met Lys Met Phe Phe Gln Gln Gln
                405                 410                 415

Ala Leu Gln Gln Asn Ser Leu Gln Gln Asn Leu Gly Asn Gln Asn Tyr
            420                 425                 430

Gln Ser Asn Thr Arg Asn Asn Thr Ala Glu Glu Thr Thr Pro Thr Asn
        435                 440                 445

Asp Asn Asn Ala Asn Gly Asn Ser Leu Leu Gln Glu His Ile Arg Ala
    450                 455                 460

Arg Phe Asn Lys Met Lys Thr Ile Pro Gln Gln Met Lys Asn Gln Ser
465                 470                 475                 480

Thr Val Ala Asn Pro Val Val Ser Asp Ile Thr Ser Gln Gln Gln Tyr
                485                 490                 495

Met His Met Met Met Gln Arg Met Ala Ala Asn Gln Gln Leu Gln Asn
            500                 505                 510

Ser Ala Phe Pro Pro Asp Thr Asn Arg Ile Ala Pro Ala Asn Asn Thr
        515                 520                 525

Met Pro Leu Gln Pro Gly Asn Met Gly Ser Pro Val Ile Glu Asn Pro
    530                 535                 540
```

```
Gly Met Arg Gln Thr Asn Pro Ser Gly Gln Asn Pro Met Ile Asn Met
545                 550                 555                 560

Gln Pro Leu Tyr Gln Asn Val Ser Ser Ala Met His Ala Phe Ala Pro
                565                 570                 575

Gln Gln Gln Phe His Leu Pro Gln His Tyr Lys Thr Asn Thr Ser Val
            580                 585                 590

Pro Gln Asn Asp Ser Thr Ser Val Phe Pro Leu Pro Asn Asn Asn Asn
        595                 600                 605

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
    610                 615                 620

Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
625                 630                 635                 640

Thr Pro Thr Val Ser Gln Pro Ser Ser Lys Cys Thr Ser Ser Ser Ser
                645                 650                 655

Thr Thr Pro Asn Ile Thr Thr Thr Ile Gln Pro Lys Arg Lys Gln Arg
            660                 665                 670

Val Gly Lys Thr Lys Thr Lys Glu Ser Arg Lys Val Ala Ala Ala Gln
        675                 680                 685

Lys Val Met Lys Ser Lys Lys Leu Glu Gln Asn Gly Asp Ser Ala Ala
    690                 695                 700

Thr Asn Phe Ile Asn Val Thr Pro Lys Asp Ser Gly Gly Lys Gly Thr
705                 710                 715                 720

Val Lys Val Gln Asn Ser Asn Ser Gln Gln Gln Lys Asn Gly Ser Phe
                725                 730                 735

Ser Met Asp Thr Glu Thr Phe Asp Ile Phe Asn Ile Gly Asp Phe Ser
            740                 745                 750

Pro Asp Leu Met Asp Ser
        755
```

<210> 32
<211> 750
<212> PRT
<213> Saccharomyces cerevisiae

<400> 32

```
Met Thr Ser Val Asn Arg Ser Asn Asn Thr Arg Ser Met Ser Ala Ser
1               5                  10                  15

Arg Ser Ala Thr Ser Arg Val Arg Asn Thr Thr Ala Asn Ser Ser Asp
            20                  25                  30

Val Asn Ser Ser Lys Arg Asn Ser Asn Ser Val Tyr Asp Asp Asn Ser
        35                  40                  45

Ser Lys Arg Arg Ser Arg Arg Ser Asp Gly Lys Asn Asn Asp His Thr
    50                  55                  60

Tyr Arg Thr Thr Val Lys Ser Lys Asn Ser Arg Tyr Val Ser Ser Ser
65                  70                  75                  80

Lys Arg Ala Lys Arg Asn Ser Val Gly Thr Ser Ser Ala Ser Lys Ser
                85                  90                  95

Ser Asn Gly Gly Ser Ala His Lys Trp Ser Asn Met Lys Asn Val Ser
            100                 105                 110

Asn Ser Ala Val Asp Ala Gly Ser Asp Ser Lys Ser Val Gly Gly Arg
        115                 120                 125

Lys Ser Asn Asn Ser Asn Asp Lys Asp Asn Ser Ala Arg Asp Asp Asn
    130                 135                 140

Asn Ser Gly Asn Asn Asn Asn Asn Asn Asn His Ser Ser Asn Asn Asn
145                 150                 155                 160

Asp Asn Asn Asn Asn Asn Asn Asp Asp Asn Asn Asn Asn Asn Asn Ser
                165                 170                 175

Asn Ser Arg Asp Asn Asn Asn Asn Ser Asp Asp Ser Asn Arg Asn Asp
            180                 185                 190

Ser Cys Lys Ala Ser Asn Lys Arg Ser Gly Ala Lys Tyr Lys Val Val
        195                 200                 205

Lys Arg Cys Ser Thr Asn Ser Thr Thr Lys Ser Trp Thr Tyr Lys Asn
    210                 215                 220

Thr Asp Val Asn Asn Tyr Val Thr Thr Thr Ala Ser His Asp Val Gly
225                 230                 235                 240

Val Tyr Arg Arg Arg Trp Val Tyr Gly Thr Thr Asp Val Lys Asn Ser
                245                 250                 255
```

```
Asn Met Asp Val Cys Cys Thr His Val Val Ser Ser Thr Met Ser Asp
            260                 265                 270

Ser Lys Tyr Ser Thr Trp Arg Gly Asp Ser Arg Met Ala Ala Tyr Ser
        275                 280                 285

Ser Asp Tyr Lys Ser Ala His Trp Tyr Thr Ala Met Lys Tyr Tyr Asn
    290                 295                 300

His Gly Lys Tyr Tyr His Met Ser Thr Val Asn Thr Ala Val Asn Gly
305                 310                 315                 320

Lys Ser Val Cys Thr Thr Ser Tyr Met Val Asp Asn Tyr Arg Ala Val
                325                 330                 335

Arg Asn Asn Gly Asn Arg Asn Ser Tyr Lys His Ser Ala Met Ser Ser
            340                 345                 350

Asp Asn Val Val Ser Tyr Lys Gly Asp Ala Asn Gly Cys Asn Asn Ala
        355                 360                 365

Asp Met Val Asn Asp Lys Tyr Arg His Gly Ser Ala Ser His Val Gly
    370                 375                 380

Gly Lys Asn Ala Lys Tyr Lys Arg Lys Asp Lys Lys Arg Lys Lys Ser
385                 390                 395                 400

Ser Asn Asn Asp Ser Ser Val Thr Ser Ser Thr Gly Asn Ser Arg Asn
                405                 410                 415

Asp Asn Asp Asp Asp Met Ser Ser Thr Thr Ser Ser Asp His Asp Ala
            420                 425                 430

Asn Asp Asp Thr Arg Arg Ser Met Thr Asn Ala Trp Thr Lys Asn Met
        435                 440                 445

Thr Ser Lys Cys Gly Val Arg Lys His Gly Gly Ala His Trp Tyr Ser
    450                 455                 460

Cys Lys Ser Ser Ser Asp Val Ser Lys Trp Met Val Lys Arg Ala Trp
465                 470                 475                 480

Asp Thr Met Val Thr Met Asn Val Val Tyr Asp Asn Thr Ser Asn Ser
                485                 490                 495

Gly Asp Cys Asp Asp Tyr Asp Lys Ser Ser Asn Gly Gly Cys Trp Gly
            500                 505                 510
```

```
Thr Trp Asp Thr Cys Lys Asn Thr His Ser Ser Ser Asp Asn Gly Lys
        515                 520                 525

Asp Tyr Met Ala Asp Ser Thr Asp Gly Asp Lys Asp Asn Gly Lys Trp
    530                 535                 540

Lys Arg Ala Cys Arg Thr Arg Ser Arg Ser Gly Val Arg Asn Asp Tyr
545                 550                 555                 560

Arg Ser Ser Asn Thr Asn Gly Ser Val Lys Cys Asn His Asn Asn Val
                565                 570                 575

Gly Ala Ser Asp Ser Ala Arg Ser Asn Asn Thr Asp His Ala Val Ser
            580                 585                 590

Val Asn Gly Asp Asn His Tyr Val Gly Tyr Lys Lys Arg Ala Asp Tyr
        595                 600                 605

Thr Cys Asp Lys Asn Gly Ser Ala Ser Tyr Thr Thr Trp Tyr Val Asn
    610                 615                 620

Ser Asn Asn Thr Asn Asp Asn Asn Tyr Asn Ser Lys Asn Gly Cys Lys
625                 630                 635                 640

Ser Asp Tyr Asp Lys Thr Thr Tyr Val Asp Ala Thr Ser Trp Arg His
                645                 650                 655

Ser Ala Arg Lys Ala Asn Arg Arg Ala Cys Thr Thr Arg Arg Lys Ser
            660                 665                 670

Lys Asp Asn Val Met Ala Ala Thr Arg Gly Thr Arg Tyr Tyr Asn Lys
        675                 680                 685

Val Arg Thr Gly Asn Val Ala Thr His Asn Thr Trp Arg Thr His Val
    690                 695                 700

Asp Val Ser Val Met Lys Ala Lys Ser Ala Ser Arg Ser Arg Arg Asn
705                 710                 715                 720

Tyr Val Val Ser Asp Asp Asp Ala Met Lys Lys Lys Ala Lys Lys Thr
                725                 730                 735

Ser Thr Arg Val Ser Cys Thr Lys Gly Arg His Cys Thr Asp
            740                 745                 750
```

<210> 33
<211> 710
<212> PRT

<213> Saccharomyces cerevisiae

<400> 33

```
Met Asp Asn Lys Arg Tyr Asn Gly Asn Ser Asn Val Asp Gly Thr Tyr
1               5                  10                  15

Asp Arg Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val
            20                  25                  30

Ser Asp Lys Arg Gly Arg Ser Ser Ser Thr Ser Lys Gly Ser Tyr Arg
        35                  40                  45

Thr Arg Ala Gly Arg Ser Asp Thr Thr Asn Ser Ser Ala Lys His His
    50                  55                  60

Ser Lys Lys Ser Thr Val Val Val Val Thr Ser Ser Thr Asp Ser Asn
65                  70                  75                  80

Ser Thr Thr Tyr Ala Arg Val Ser Ser Asp Ser Thr Val Ala Thr Ser
                85                  90                  95

Ser Thr Thr Thr Arg Thr Arg Thr Arg Asn Asn Thr Val Ser Ser Thr
            100                 105                 110

Ala Ser Ser Ser Thr Thr Asp Val Gly Asn Ala Thr Ser Ala Asn Trp
        115                 120                 125

Ser Ala Asn Ala Ser Asn Thr Ser Ser Ser Asp Tyr Ala Thr Ser Tyr
    130                 135                 140

Thr Arg Lys Ser Thr Asp Asn Tyr Thr Thr Ala Asn Ser Lys Asn Gly
145                 150                 155                 160

Asn Asn Trp Ser Ser Ala Gly Asn Ser Asn Thr Asp His Asn Thr Val
                165                 170                 175

Asn Arg Arg Ser Ser Ser Thr Thr Asn Arg Val Tyr Thr Asp Ala Tyr
            180                 185                 190

Tyr Ala Asn Tyr Val Val Arg Val Lys Ser Thr Ser Ser Val Asp Asp
        195                 200                 205

Val Asp Ala Ser Asn Trp Thr Ala Asn Lys Val Val Asn Ser Ala Thr
    210                 215                 220

Asn Thr Ser Ser Asn Val Thr His Asn Ala Val Asn Thr Ser Thr Ser
225                 230                 235                 240
```

```
Ala Thr Cys Ser Tyr Gly Lys Val Ser Ala Arg Thr Arg Gly Asn Met
                245                 250                 255

Ala Val Ser Thr Val Ser Ala Cys Ala Ala Gly Lys Ser Lys Val Gly
            260                 265                 270

Ala Ser Thr Val Ser Ala Arg Val Met Tyr Asn Val Asn Gly Asn Asn
        275                 280                 285

Thr Lys Asn His Gly Val Asn Tyr Ser Thr Ser Asn Asn Thr Tyr Cys
    290                 295                 300

Asn Thr Asn Ser His Ser Ser Asn Asn Tyr Ser Ser Asp Ser Lys Lys
305                 310                 315                 320

Asp His Thr Ser Ser Lys Tyr Asp His Asn His Asn Ala Lys Asn Lys
                325                 330                 335

Gly Val Ser Asp Thr Asn Tyr Gly His Asn Ser Lys Val Lys Arg Lys
            340                 345                 350

Asp Thr Asp Ala Lys Arg Arg Lys Asp Ser Asn Ser Ser Thr Met Ala
        355                 360                 365

Val Met Asp Ser Ser Asp Tyr Gly Asn Thr Val Lys Asn Ser Ser Asn
    370                 375                 380

Arg Asp Met Arg Lys Cys Asn Lys Tyr Thr Ser Met Gly Val His Lys
385                 390                 395                 400

Asn Gly Thr Trp Val Cys Lys Lys Met Ala Asn Thr Arg Asn Val Thr
                405                 410                 415

Ser Gly Val Ser Asp Tyr Cys Thr Asn Asp Gly Asn Tyr Val Gly Lys
            420                 425                 430

Gly Trp Asn Ser Ser Val Ser His Trp Thr Val Asn Arg Tyr Gly Ser
        435                 440                 445

Arg Ala Val Arg Ala Cys Ala Asp Ser Thr Cys Thr Thr Ser Val Ser
    450                 455                 460

Tyr Ala Thr Asp Thr Asn Gly Thr Thr Trp Asp Thr Cys Thr Asn Lys
465                 470                 475                 480

Asn Cys Asp Lys Val Asn Lys Asn Val Lys Cys Cys His Lys Gly Ser
                485                 490                 495
```

```
Thr Cys Lys Asn Arg Gly Gly Ala Ser Lys Asn Lys His Ala Asp Gly
            500                 505                 510

Ser Ser Asp Ser Asp Gly Asn Tyr Gly Thr Tyr Lys Val Thr Ser Arg
        515                 520                 525

Asp Asn Ser Val Arg Asp Ala Thr Lys Arg Asn Ser Asn Asn Ser Arg
    530                 535                 540

Val Gly Ser Ser Ala Gly Ser Lys Ser Ser Lys Asn His Gly Lys His
545                 550                 555                 560

Gly His Ser Gly Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser
                565                 570                 575

Ser Asn Ser Arg His Asn Ser Val Met Asn Asn Ala Gly Thr Ala Asn
            580                 585                 590

Asn Ala Met Ser Asn Ser Tyr Asn Asn Val Val Tyr Ser Gly Asn Asn
        595                 600                 605

Asn Asn Gly Asn Ser Asn Gly Asp Asn Ser Asp Ser Arg Ala Asn Gly
    610                 615                 620

Thr Asn Ser Val Asn Asn Val Ser Asn Asn Asn Asn Asn Tyr Asn Asn
625                 630                 635                 640

Ser Gly Tyr Ser Ser Met Asn Ser Arg Ser Val Ser His Asn Asn Asn
                645                 650                 655

Asn Asn Thr Asn Asn Thr Asn Asn Asn Asp Asn Asp Asn Asn Asn Asn
            660                 665                 670

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
        675                 680                 685

Asn Ser Asn Asn Ser Asn Asn Asn Asn Asn Asn Asp Thr Ser Tyr Arg
    690                 695                 700

Tyr Arg Ser Tyr Gly Tyr
705                 710
```

<210> 34
<211> 477
<212> PRT
<213> Saccharomyces cerevisiae

<400> 34

```
Asp Thr Lys Gly Tyr Asp Asp Asp Ala Ala Thr Asp Gly Lys Lys His
1               5                  10                  15

Arg Arg Tyr Arg Tyr Val Ser Gly Ser Val Ser Gly Lys Arg Trp Thr
            20                  25                  30

Asp Gly Val Ser Trp Ser Ser Arg Ser Gly Lys Tyr Lys Asp Lys Asn
        35                  40                  45

Ala Gly Ser Asn Ala Asn Ala Thr Ser Ser Gly Ser Thr Asp Ser Ala
    50                  55                  60

Val Thr Asp Gly Thr Ser Gly Ala Arg Asn Asn Ser Ser Ser Lys Lys
65                  70                  75                  80

Lys Asn His Asp Thr Met Gly His Ser Ser Ser Asp Thr Ser Ser Ser
                85                  90                  95

Asn Arg Ser Asn Lys Tyr Thr Gly Val Lys Lys Thr Ser Val Lys Lys
            100                 105                 110

Arg Asn Ser Asn His Val Ser Tyr Tyr Ser Val Lys Asp Lys Asn Cys
        115                 120                 125

Val Thr Lys Ala Ser Lys Asp Val Arg Ser Val Ala Met Gly Asn Thr
    130                 135                 140

Thr Gly Asn Val Lys Asn Asn Ser Thr Thr Thr Gly Asn Gly Asn Asn
145                 150                 155                 160

Asn Asn Lys Ser Asn Ser Ser Thr Asn Thr Val Ser Thr Asn Asn Asn
                165                 170                 175

Ser Ala Asn Asn Ala Ala Gly Ser Asn Thr Ser Ala Asn Lys Asn Tyr
            180                 185                 190

Tyr Tyr Lys Asn Asp Ser Ser Gly Tyr Thr Ala Ala Ser Thr Thr Met
        195                 200                 205

Tyr Thr Ala Asn Tyr Thr Ser Asp Asn Thr Asn Ala Thr Gly Met Asn
    210                 215                 220

Thr His Val Asn Asn Asn Asn Asn Asn Ser Asn Asn Ser Ser Asn Ser
225                 230                 235                 240

Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
                245                 250                 255
```

```
Asn Asn Asn Asn Asn Asn Asn Asn Val Asn Thr Asn Ala Gly Asn Gly
            260                 265                 270

Asn Asn Asn Arg His Asn Ala Ser Ala Tyr Asn Thr Thr Gly Asp Asn
        275                 280                 285

Gly Ser Tyr Tyr Tyr Thr Thr Asn Asn Asn Tyr Tyr Thr Thr Asn Val
    290                 295                 300

Thr Asn Ala Ser Thr Asn Asn Gly Tyr Ser Thr Ser Ser Thr His Tyr
305                 310                 315                 320

Tyr Gly His Thr Ser Ser Ala Ser Ala Ala Ala Gly Ala Thr Gly Thr
                325                 330                 335

Gly Thr Ala Asn Val Val Ser Ser Met His Ala Asn Asn Asn Ser Ala
            340                 345                 350

Ser Ser Ala Thr Ser Thr Ala Tyr Val Tyr Ser Met Asn Val Asn Val
        355                 360                 365

Tyr Tyr Asn Ser Ser Ala Ser Ala Tyr Lys Arg Ala Asn Thr Thr Ser
    370                 375                 380

Asn Thr Asn Ala Ser Gly Ala Thr Ser Thr Asn Ser Gly Thr Met Ser
385                 390                 395                 400

Asn Ala Tyr Ala Asn Ser Tyr Thr Ser Val Tyr Tyr Gly Tyr Ala Met
                405                 410                 415

Ala Ser Ala Asn Ser Met Tyr His His His Thr Val Tyr Ala Thr Asn
            420                 425                 430

Met Ser Ser Gly His Thr Ser Thr Gly Ser Asp His His His Tyr Asn
        435                 440                 445

Asp His Lys Asn Ala Met Gly His Ala Asn Asn Asn Asn Thr Asn Asn
    450                 455                 460

Asp Thr Met Asn Asn Asn Thr Asn Thr Ser Thr Thr Thr
465                 470                 475
```

<210> 35
<211> 454
<212> PRT
<213> Saccharomyces cerevisiae

<400> 35

```
Met Asp Val Arg Ala Ala Cys Ser Ala Ser Gly Arg Thr Gly Lys Lys
1               5                  10                  15

Gly Tyr Ser Tyr Lys Met Ser Asn Ser Gly Gly Ser Ser Ser Gly Gly
            20                  25                  30

Ser Asp Val Gly Ser Thr Asn Gly Ser Asn Arg Ala Lys Asn Thr Asn
        35                  40                  45

Tyr Lys Lys Thr Asn Lys Lys Tyr Lys Ala Thr Asp Lys Ala Asn Asp
    50                  55                  60

Thr Lys Tyr Tyr Ser Asn Asp Lys Lys Ser Lys Arg Ser Ala Asn Ser
65                  70                  75                  80

Met Asn Asp Lys Asp Lys Cys Arg Thr Thr Asn Lys Asp Met Thr Arg
                85                  90                  95

Tyr Asp Ser Lys Ser Lys Val Thr Asn Cys Asp His Lys Ala Ser Ser
            100                 105                 110

His Ser Met Lys Tyr Lys Lys Arg Ser Val Asp Lys Asp His Val Met
        115                 120                 125

Lys Asp Asp Ser Ser Val Lys Ala Ser Lys Met Asn Ser His Asn Tyr
    130                 135                 140

Ser Thr Asn Thr Met Asn Lys Met Asp Val Tyr Thr Lys Ala Asn Met
145                 150                 155                 160

Ala Asn Lys Lys Lys Ser Asp Thr Ser Thr Trp Lys Asn Lys Asn Lys
                165                 170                 175

Ser His Val Ser Tyr Asn Asn Asp Lys Ser Lys Thr Lys Trp Tyr Asn
            180                 185                 190

Asp Ser Asp Asp Asp Asp Asp Asn Asn Val Asn Asn Asn Asp Asn Asn
        195                 200                 205

Asn Asn Asn Lys Asn Asp Asn Asn Asn Asp Asn Asn Asn Asp Thr Ser
    210                 215                 220

Asn Asn Asn Asn Asn Asn Asn Asn Arg Thr Lys Asn Asn Arg Asn Asn
225                 230                 235                 240

Arg Asp Trp Lys Thr Lys Lys Cys Thr Asp Met Asn Asp Lys Arg Asp
                245                 250                 255
```

```
Asn Asn Asn Lys Asn Asp Met Ala Arg Asn Asp Asn Lys Asn Tyr Asn
            260                 265                 270

Asn Val Asn Lys Arg Asn His Lys Ser Ser Cys Arg Arg Asp Gly Tyr
        275                 280                 285

Ser Ala Asn Asn Ala Val Asn Ser Thr His Ala Ser Asn Lys Asn Val
    290                 295                 300

Asn Asp Met Asn Asn Asp Thr Tyr Lys Asn Lys Thr Asp Thr Asn Lys
305                 310                 315                 320

Lys Asn Asp Ser Asn Ser Asn Asp Val Thr Arg Lys Lys Arg Lys Thr
                325                 330                 335

Ser Asp Gly Asn Tyr Ser Arg Asn Asn Val Ser Val Ser Arg Ser Lys
            340                 345                 350

Ala Thr Thr Lys Lys Thr Lys Lys Lys Lys Arg Arg Asp Gly Lys Asp
        355                 360                 365

Lys Lys Asn Lys Lys Asn Ala Asp Asn Lys Lys Asn Asn Ala Val Thr
    370                 375                 380

Val Ser Val Tyr Asp Ser Asn Lys Val Lys Ser Asn Lys Arg Ser Arg
385                 390                 395                 400

Lys Val Asn Asn Lys Ser Asp Val Val Asn Ser Gly Lys Asp Ser Arg
                405                 410                 415

Val Lys Ser Cys Lys Lys Tyr Ala Asp Asn Asn Thr Lys Ser Asn Asp
            420                 425                 430

Ala Asp Gly Trp Asp Asp Met Asn Trp Val Asp Arg Gly Cys Ala Thr
        435                 440                 445

Thr Arg Trp Arg Ala Lys
    450
```

<210> 36
<211> 284
<212> PRT
<213> Saccharomyces cerevisiae

<400> 36

```
Met Asn Val Thr Ser Lys Asp Gly Asn His Ser Ser Lys Lys Asn Arg
1               5                   10                  15
```

Asn Thr Asn Lys Arg His Lys Asn Ala Ser Asn Asp Arg Asp Ser Val
20 25 30

Ser Ser Asn Thr Thr Ser Met Thr Asp Asp Ala Asp Tyr Asn Gly Ala
35 40 45

Ser Arg Thr Lys Asn Asn Ser Asp Ser Asp Arg Ser Asn Asp Thr Lys
50 55 60

Asn Asn Tyr Asn Lys Arg Thr Gly Tyr Asn Tyr Asn Gly Ser Gly Asn
65 70 75 80

Arg Tyr Thr Arg Lys Arg Thr Ala Asn Lys Ala Tyr Ser Asp Asp Asn
85 90 95

Val Lys Asp Asp Asn Asn Thr Lys Lys Ala Ser Arg Ser Ser Gly Arg
100 105 110

Asn Val Asn Thr Arg Asn Lys Ser Lys Ser His Lys Val Lys Asn Asn
115 120 125

Lys Ser Ser Ser Arg Lys Ser Ser Ala Ala Arg Lys Gly Lys Tyr Asn
130 135 140

Ser Asn Ser Asp Ser Thr Thr Arg Lys Val Thr Asp Val Lys Lys Arg
145 150 155 160

Ser Lys Trp His Arg His Asp Lys Lys Met Val Lys Lys Ser Arg Tyr
165 170 175

Arg Lys Arg Met Arg Gly Thr Asp Val Ser Ser Ser Asp Asn Ser Lys
180 185 190

Ser Thr Thr Lys Ser Tyr Val Ser Lys Asn Ser Ala Met Asn Asn Asn
195 200 205

Asp Val Thr Asp Asn Lys Lys Thr Asn Asn Asn Lys Ala Arg Asp Ser
210 215 220

Met His Thr Lys Lys Asp Thr Lys Asp Asp Thr Asp Ser Lys Lys Arg
225 230 235 240

Lys Val Val Thr Asn Asp Asn Ala Ala Met Val Asn Lys Gly Trp Arg
245 250 255

Lys Asn Val Met Met Tyr Lys Lys Ser Gly Asn Met Lys Lys Tyr Arg
260 265 270

```
Tyr Trp Thr Cys Tyr Cys Asn Tyr Val Tyr Tyr Arg
        275                 280
```

<210> 37
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 37
gggaattccc attaccgaca tttgggcgc 29

<210> 38
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 38
ggggattctg attgattgat tgattgtac 29

<210> 39
<211> 720
<212> DNA
<213> Artificial sequence

<220>
<223> Superbright GFP encoding sequence

<220>
<221> CDS
<222> (1)..(720)

<400> 39

```
atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt      48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                  10                  15

gtt gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc act tat ggt gtt cag tgc ttt tca aga tac ccg gat cat atg aaa     240
Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa     288
```

```
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

aga act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

att gat ttt aaa gaa gat gga aac att ctt ggg cac aaa ttg gaa tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

gga atc aaa gct aac ttc aaa att aga cac aac att gaa gat gga agc      528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc      576
Val Gln Leu Ala Asp His tyr Gln Gln Asn thr Pro Ile Gly Asp gly
            180                 185                 190

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt      624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt      672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu glu Phe
    210                 215                 220

gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa tga      720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp glu Leu Tyr Lys
225                 230                 235                 240
```

<210> 40
<211> 239
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Peptide

<400> 40

```
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
```

50 55 60

Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 41
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 41
gaccgcggat ggctagcaaa ggagaag 27

<210> 42
<211> 28
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 42
cctgagctct catttgtata gttcatcc 28

<210> 43
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 43
ggaggatcca tggatacgga taagttaatc tcag 34

<210> 44
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 44
ggaccgcggg tagcggttct gttgagaaaa gttgcc 36

<210> 45
<211> 7239
<212> DNA
<213> Artificial sequence

<220>
<223> Vector containing chimeric gene

<400> 45
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atttcaacaa aaagcgtact ttacatatat atttattaga caagaaaagc agattaaata 300

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<211> 741
<212> PRT
<213> Pichia pinus

<400> 46

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Ala Gly Asn Val Gln Asn Ile Asn Leu Asn Ala Pro Ala Tyr Asp Pro
20 25 30

Ala Val Gln Ser Tyr Ile Pro Asn Thr Ala Gln Ala Phe Val Pro Ser
35 40 45

Ala Gln Pro Tyr Ile Pro Gly Gln Gln Glu Gln Gln Phe Gly Gln Tyr
50 55 60

Gly Gln Gln Gln Gln Asn Tyr Asn Gln Gly Gly Tyr Asn Asn Tyr Asn
65 70 75 80

Asn Arg Gly Gly Tyr Ser Asn Asn Arg Gly Gly Tyr Asn Asn Ser Asn
85 90 95

Arg Gly Gly Tyr Ser Asn Tyr Asn Ser Tyr Asn Thr Asn Ser Asn Gln
100 105 110

Gly Gly Tyr Ser Asn Tyr Asn Asn Asn Tyr Ala Asn Asn Ser Tyr Asn

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        115                 120                 125

Asn Asn Asn Asn Tyr Asn Asn Asn Tyr Asn Gln Gly Tyr Asn Asn Tyr
    130                 135                 140

Asn Ser Gln Pro Gln Gly Gln Asp Gln Gln Gln Glu Thr Gly Ser Gly
145                 150                 155                 160

Gln Met Ser Leu Glu Asp Tyr Gln Lys Gln Gln Lys Glu Ser Leu Asn
                165                 170                 175

Lys Leu Asn Thr Lys Pro Lys Lys Val Leu Lys Leu Asn Leu Asn Ser
            180                 185                 190

Ser Thr Val Lys Ala Pro Ile Val Thr Lys Lys Lys Glu Glu Glu Pro
        195                 200                 205

Val Asn Gln Glu Ser Lys Thr Glu Glu Pro Ala Lys Glu Glu Ile Lys
    210                 215                 220

Asn Gln Glu Pro Ala Glu Ala Glu Asn Lys Val Glu Glu Glu Ser Lys
225                 230                 235                 240

Val Glu Ala Pro Thr Ala Ala Lys Pro Val Ser Glu Ser Glu Phe Pro
                245                 250                 255

Ala Ser Thr Pro Lys Thr Glu Ala Lys Ala Ser Lys Glu Val Ala Ala
            260                 265                 270

Ala Ala Ala Ala Leu Lys Lys Glu Val Ser Gln Ala Lys Lys Glu Ser
        275                 280                 285

Asn Val Thr Asn Ala Asp Ala Leu Val Lys Glu Gln Glu Glu Gln Ile
    290                 295                 300

Asp Ala Ser Ile Val Asn Asp Met Phe Gly Gly Lys Asp His Met Ser
305                 310                 315                 320

Ile Ile Phe Met Gly His Val Asp Ala Gly Lys Ser Thr Met Gly Gly
                325                 330                 335

Asn Leu Leu Phe Leu Thr Gly Ala Val Asp Lys Arg Thr Val Glu Lys
            340                 345                 350

Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg Gln Gly Trp Tyr Leu Ser
        355                 360                 365
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Trp Ile Met Asp Thr Asn Lys Glu Glu Arg Asn Asp Gly Lys Thr Ile
    370                 375                 380

Glu Val Gly Lys Ser Tyr Phe Glu Thr Asp Lys Arg Arg Tyr Thr Ile
385                 390                 395                 400

Leu Asp Ala Pro Gly His Lys Leu Tyr Ile Ser Glu Met Ile Gly Gly
                405                 410                 415

Ala Ser Gln Ala Asp Val Gly Val Leu Val Ile Ser Ser Arg Lys Gly
            420                 425                 430

Glu Tyr Glu Ala Gly Phe Glu Arg Gly Gly Gln Ser Arg Glu His Ala
        435                 440                 445

Ile Leu Ala Lys Thr Gln Gly Val Asn Lys Leu Val Val Val Ile Asn
    450                 455                 460

Lys Met Asp Asp Pro Thr Val Asn Trp Ser Lys Glu Arg Tyr Glu Glu
465                 470                 475                 480

Cys Thr Thr Lys Leu Ala Met Tyr Leu Lys Gly Val Gly Tyr Gln Lys
                485                 490                 495

Gly Asp Val Leu Phe Met Pro Val Ser Gly Tyr Thr Gly Ala Gly Leu
            500                 505                 510

Lys Glu Arg Val Ser Gln Lys Asp Ala Pro Trp Tyr Asn Gly Pro Ser
        515                 520                 525

Leu Leu Glu Tyr Leu Asp Ser Met Pro Leu Ala Val Arg Lys Ile Asn
    530                 535                 540

Asp Pro Phe Met Leu Pro Ile Ser Ser Lys Met Lys Asp Leu Gly Thr
545                 550                 555                 560

Val Ile Glu Gly Lys Ile Glu Ser Gly His Val Lys Lys Gly Gln Asn
                565                 570                 575

Leu Leu Val Met Pro Asn Lys Thr Gln Val Glu Val Thr Thr Ile Tyr
            580                 585                 590

Asn Glu Thr Glu Ala Glu Ala Asp Ser Ala Phe Cys Gly Glu Gln Val
        595                 600                 605

Arg Leu Arg Leu Arg Gly Ile Glu Glu Glu Asp Leu Ser Ala Gly Tyr
    610                 615                 620
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Val Leu Ser Ser Ile Asn His Pro Val Lys Thr Val Thr Arg Phe Glu
625                 630                 635                 640

Ala Gln Ile Ala Ile Val Glu Leu Lys Ser Ile Leu Ser Thr Gly Phe
                645                 650                 655

Ser Cys Val Met His Val His Thr Ala Ile Glu Glu Val Thr Phe Thr
            660                 665                 670

Gln Leu Leu His Asn Leu Gln Lys Gly Thr Asn Arg Arg Ser Lys Lys
        675                 680                 685

Ala Pro Ala Phe Ala Lys Gln Gly Met Lys Ile Ile Ala Val Leu Glu
    690                 695                 700

Thr Thr Glu Pro Val Cys Ile Glu Ser Tyr Asp Asp Tyr Pro Gln Leu
705                 710                 715                 720

Gly Arg Phe Thr Leu Arg Asp Gln Gly Gln Thr Ile Ala Ile Gly Lys
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Val Thr Lys Leu Leu
            740
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<211> 715
<212> PRT
<213> Candida albicans

<400> 47

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Met Ala Asn Ala Ser Leu Asn Gly Asp Gln Ser Lys Gln Gln Gln Gln
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Gln Gln Gln Gln Gln Gln Gln Gln Gln Asn Tyr Tyr Asn Pro Asn Ala
            20                  25                  30

Ala Gln Ser Phe Val Pro Gln Gly Gly Tyr Gln Gln Phe Gln Gln Phe
        35                  40                  45

Gln Pro Gln Gln Gln Gln Gln Gln Tyr Gly Gly Tyr Asn Gln Tyr Asn
    50                  55                  60

Gln Tyr Gln Gly Gly Tyr Gln Gln Asn Tyr Asn Asn Arg Gly Gly Tyr
65                  70                  75                  80

Gln Gln Gly Tyr Asn Asn Arg Gly Gly Tyr Gln Gln Asn Tyr Asn Asn
                85                  90                  95
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Arg Gly Gly Tyr Gln Gly Tyr Asn Gln Asn Gln Gln Tyr Gly Gly Tyr
            100                 105                 110

Gln Gln Tyr Asn Ser Gln Pro Gln Gln Gln Gln Gln Gln Ser Gln
        115                 120                 125

Gly Met Ser Leu Ala Asp Phe Gln Lys Gln Lys Thr Glu Gln Gln Ala
    130                 135                 140

Ser Leu Asn Lys Pro Ala Val Lys Lys Thr Leu Lys Leu Ala Gly Ser
145                 150                 155                 160

Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Asp Thr Thr Ser
                165                 170                 175

Lys Pro Gln Ser Lys Glu Ser Ser Pro Ala Pro Ala Pro Ala Ala Ser
            180                 185                 190

Ala Ser Ala Ser Ala Pro Gln Glu Glu Lys Lys Glu Glu Lys Glu Ala
        195                 200                 205

Ala Ala Ala Thr Pro Ala Ala Ala Pro Glu Thr Lys Lys Glu Thr Ser
    210                 215                 220

Ala Pro Ala Glu Thr Lys Lys Glu Ala Thr Pro Thr Pro Ala Ala Lys
225                 230                 235                 240

Asn Glu Ser Thr Pro Ile Pro Ala Ala Ala Ala Lys Lys Glu Ser Thr
                245                 250                 255

Pro Cys Ser Asn Ser Ala Ser Val Ala Thr Ala Asp Ala Leu Val Lys
            260                 265                 270

Glu Gln Glu Asp Glu Ile Asp Glu Glu Val Val Lys Asp Met Phe Gly
        275                 280                 285

Gly Lys Asp His Val Ser Ile Ile Phe Met Gly His Val Asp Ala Gly
    290                 295                 300

Lys Ser Thr Met Gly Gly Asn Ile Leu Tyr Leu Thr Gly Ser Val Asp
305                 310                 315                 320

Lys Arg Thr Val Glu Lys Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg
                325                 330                 335

Gln Gly Trp Tyr Leu Ser Trp Val Met Asp Thr Asn Lys Glu Glu Arg
            340                 345                 350
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Asn Asp Gly Leu Thr Ile Glu Val Gly Lys Ala Tyr Phe Glu Thr Asp
        355                 360                 365

Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly His Lys Met Tyr Val
    370                 375                 380

Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp Val Gly Ile Leu Val
385                 390                 395                 400

Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly Phe Glu Lys Gly Gly
                405                 410                 415

Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr Gln Gly Val Asn Lys
            420                 425                 430

Ile Ile Val Val Val Asn Lys Met Asp Asp Ser Thr Val Gly Trp Ser
        435                 440                 445

Lys Glu Arg Tyr Gln Glu Cys Thr Thr Lys Leu Gly Ala Phe Leu Lys
    450                 455                 460

Gly Ile Gly Tyr Ala Lys Asp Asp Ile Ile Tyr Met Pro Val Ser Gly
465                 470                 475                 480

Tyr Thr Gly Ala Gly Leu Lys Asp Arg Val Asp Pro Lys Asp Cys Pro
                485                 490                 495

Trp Tyr Asp Gly Pro Ser Leu Leu Glu Tyr Leu Asp Asn Met Asp Thr
            500                 505                 510

Met Asn Arg Lys Ile Asn Gly Pro Phe Met Met Pro Val Ser Gly Lys
        515                 520                 525

Met Lys Asp Leu Gly Thr Ile Val Glu Gly Lys Ile Glu Ser Gly His
    530                 535                 540

Val Lys Lys Gly Thr Asn Leu Ile Met Met Pro Asn Lys Thr Pro Ile
545                 550                 555                 560

Glu Val Leu Thr Ile Phe Asn Glu Thr Glu Gln Glu Cys Asp Thr Ala
                565                 570                 575

Phe Ser Gly Glu Gln Val Arg Leu Lys Ile Lys Gly Ile Glu Glu Glu
            580                 585                 590

Asp Leu Gln Pro Gly Tyr Val Leu Thr Ser Pro Lys Asn Pro Val Lys
        595                 600                 605
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Thr Val Thr Arg Phe Glu Ala Gln Ile Ala Ile Val Glu Leu Lys Ser
    610                 615                 620

Ile Leu Ser Asn Gly Phe Ser Cys Val Met His Leu His Thr Ala Ile
625                 630                 635                 640

Glu Glu Val Lys Phe Ile Glu Leu Lys His Lys Leu Glu Lys Gly Thr
                645                 650                 655

Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe Ala Lys Lys Gly Met Lys
            660                 665                 670

Ile Ile Ala Ile Leu Glu Val Gly Glu Leu Val Cys Ala Glu Thr Tyr
        675                 680                 685

Leu Asp Tyr Pro Gln Leu Gly Arg Phe Thr Leu Arg Asp Gln Gly Thr
    690                 695                 700

Thr Ile Ala Ile Gly Lys Ile Thr Lys Leu Leu
705                 710                 715
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<212> DNA
<213> Saccharomyces cerevisiae

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gtttattcct ggcatccact aaatataatg gagcccgctt tttaagctgg catccagaaa 240

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atggagtgat gcaacctgcc tggagtaaat gatgacacaa ggcaattgac ccacgcatgt 420

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gaaaaaaaag gtttaaacca gttccctgaa attattcccc tacttgacta ataagtatat 540

aaagacggta ggtattgatt gtaattctgt aaatctattt cttaaacttc ttaaattcta 600

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<212> DNA
<213> Artificial sequence

<220>

<223> Ure2N-Sup35C integration plasmid

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accataccac agcttttcaa ttcaattcat catttttttt ttattctttt ttttgatttc 240

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Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
35 40 45

Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
50 55 60

Gln Asp Arg Ala Ala Gly Gly Gly Ser Ser Phe Met Asn Thr Leu Met
65 70 75 80

Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
85 90 95

Leu Ala Thr Val Met Thr His Ser Ser Asn Lys Gly Ser Ser Asn Arg
100 105 110

Gly Phe Asp Val Gly Thr Val Met Ser Met Leu Ser Gly Ser Gly Gly
115 120 125

Gly Ser Gln Ser Met Gly Ala Ser Gly Leu Ala Ala Leu Ala Ser Gln
130 135 140

Phe Phe Lys Ser Gly Asn Asn Ser Gln Gly Gln Gly Gln Gly Gln Gly
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Leu Ala Ser Leu Ala Ser Ser Phe Met Asn Ser Asn Asn Asn Asn Gln
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Gln Gly Gln Asn Gln Ser Ser Gly Gly Ser Ser Phe Gly Ala Leu Ala
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Ser Met Ala Ser Ser Phe Met His Ser Asn Asn Asn Gln Asn Ser Asn
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Asn Ser Gln Gln Gly Tyr Asn Gln Ser Tyr Gln Asn Gly Asn Gln Asn
225                 230                 235                 240

Ser Gln Gly Tyr Asn Asn Gln Gln Tyr Gln Gly Gly Asn Gly Gly Tyr
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Gln Gln Gln Gln Gly Gln Ser Gly Gly Ala Phe Ser Ser Leu Ala Ser
            260                 265                 270

Met Ala Gln Ser Tyr Leu Gly Gly Gly Gln Tyr Gln Ser Asn Gln Gln
        275                 280                 285

Gln Tyr Asn Gln Gln Gly Gln Asn Asn Gln Gln Gln Tyr Gln Gln Gln
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Gly Gln Asn Tyr Gln His Gln Gln Gln Gly Gln Gln Gln Gln Gln Gly
305                 310                 315                 320

His Ser Ser Ser Phe Ser Ala Leu Ala Ser Met Ala Ser Ser Tyr Leu
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Gly Asn Asn Ser Asn Ser Asn Ser Ser Tyr Gly Gly Gln Gln Gln Ala
            340                 345                 350

Asn Glu Tyr Gly Arg Pro Gln His Asn Gly Gln Gln Gln Ser Asn Glu
        355                 360                 365

Tyr Gly Arg Pro Gln Tyr Gly Gly Asn Gln Asn Ser Asn Gly Gln His
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Glu Ser Phe Asn Phe Ser Gly Asn Phe Ser Gln Gln Asn Asn Asn Gly
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Thr Gln Glu Arg Gly Tyr Pro Pro Gln Gln Gln Gln Gln Tyr Tyr Gln
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Gln Gln Gln Gln His Pro Gly Tyr Tyr Asn Gln Gln Gly Tyr Asn Gln
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Gln Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln
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Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln Gly His Gln Gln Pro Val
85 90 95

Tyr Val Gln Gln Gln Pro Pro Gln Arg Gly Asn Glu Gly Cys Leu Ala
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<213> Saccharomyces cerevisiae

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Gly Ser Gly Thr Ser Gln Leu Asp Gln Leu Ala Ala Leu Gln Ala Leu
35 40 45

Ser Ser Ser Leu Asn Lys Leu Asn Asn Pro Asn Ser Asn Asn Ser Ser
50 55 60

Ser Asn Asn Ser Asn Gln Asp Thr Ser Ser Ser Lys Gln Asp Gly Thr

65 70 75 80

Ala Asn Asp Lys Glu Gly Ser Asn Glu Asp Thr Lys Asn Glu Lys Lys
85 90 95

Gln Glu Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn Ala Ser Ser Ala
100 105 110

Gly Pro Ser Gly Leu Pro Trp Glu Gln Leu Gln Gln Thr Met Ser Gln
115 120 125

Phe Gln Gln Pro Ser Ser Gln Ser Pro Pro Gln Gln Gln Val Thr Gln
130 135 140

Thr Lys Glu Glu Arg Ser Lys Ala Asp Leu Ser Lys Glu Ser Cys Lys
145 150 155 160

Met Phe Ile Gly Gly Leu Asn Trp Asp Thr Thr Glu Asp Asn Leu Arg
165 170 175

Glu Tyr Phe Gly Lys Tyr Gly Thr Val Thr Asp Leu Lys Ile Met Lys
180 185 190

Asp Pro Ala Thr Gly Arg Ser Arg Gly Phe Gly Phe Leu Ser Phe Glu
195 200 205

Lys Pro Ser Ser Val Asp Glu Val Val Lys Thr Gln His Ile Leu Asp
210 215 220

Gly Lys Val Ile Asp Pro Lys Arg Ala Ile Pro Arg Asp Glu Gln Asp
225 230 235 240

Lys Thr Gly Lys Ile Phe Val Gly Gly Ile Gly Pro Asp Val Arg Pro
245 250 255

Lys Glu Phe Glu Glu Phe Phe Ser Gln Trp Gly Thr Ile Ile Asp Ala
260 265 270

Gln Leu Met Leu Asp Lys Asp Thr Gly Gln Ser Arg Gly Phe Gly Phe
275 280 285

Val Thr Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Gln Asn Lys
290 295 300

Phe Ile Asp Phe Lys Asp Arg Lys Ile Glu Ile Lys Arg Ala Glu Pro
305 310 315 320

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Arg His Met Gln Gln Lys Ser Ser Asn Asn Gly Gly Asn Asn Gly Gly
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Asn Asn Met Asn Arg Arg Gly Gly Asn Phe Gly Asn Gln Gly Asp Phe
            340                 345                 350

Asn Gln Met Tyr Gln Asn Pro Met Met Gly Gly Tyr Asn Pro Met Met
        355                 360                 365

Asn Pro Gln Ala Met Thr Asp Tyr Tyr Gln Lys Met Gln Glu Tyr Tyr
    370                 375                 380

Gln Gln Met Gln Lys Gln Thr Gly Met Asp Tyr Thr Gln Met Tyr Gln
385                 390                 395                 400

Gln Gln Met Gln Gln Met Ala Met Met Met Pro Gly Phe Ala Met Pro
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Pro Asn Ala Met Thr Leu Asn Gln Pro Gln Gln Asp Ser Asn Ala Thr
            420                 425                 430

Gln Gly Ser Pro Ala Pro Ser Asp Ser Asp Asn Asn Lys Ser Asn Asp
        435                 440                 445

Val Gln Thr Ile Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Pro Pro
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Leu Asn Leu Pro Asn Gly Pro Lys Gly Pro Ser Gln Tyr Asn Asp Asp
465                 470                 475                 480

His Asn Ser Gly Tyr Gly Tyr Asn Arg Asp Arg Gly Asp Arg Asp Arg
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Asn Asp Arg Asp Arg Asp Tyr Asn His Arg Ser Gly Gly Asn His Arg
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agtaaagaca caaacgagag tccctggaga tcagatctgt tgatagatga aaacttgctt 1500

tctcctttgg cgggagaaga tgatccattc cttctcgaag ggaacacgaa tgaggattgt 1560

aagcctctta ttttaccgga cactaaacct aaaattaagg atactggaga tacaatctta 1620

tcaagtccca gcagtgtggc actaccccaa gtgaaaacag aaaaagatga tttcattgaa 1680

ctttgcaccc ccggggtaat taagcaagag aaactgggcc cagtttattg tcaggcaagc 1740

ttttctggga caaatataat tggtaataaa atgtctgcca tttctgttca tggtgtgagt 1800

acctctggag gacagatgta ccactatgac atgaatacag catccctttc tcagcagcag 1860

gatcagaagc ctgtttttaa tgtcattcca ccaattcctg ttggttctga aaactggaat 1920

aggtgccaag gctccggaga ggacagcctg acttccttgg gggctctgaa cttcccaggc 1980

cggtcagtgt tttctaatgg gtactcaagc cctggaatga gaccagatgt aagctctcct 2040

ccatccagct cgtcagcagc cacgggacca cctcccaagc tctgcctggt gtgctccgat 2100

gaagcttcag gatgtcatta cggggtgctg acatgtggaa gctgcaaagt attctttaaa 2160

agagcagtgg aaggacagca caattacctt tgtgctggaa gaaacgattg catcattgat 2220

aaaattcgaa ggaaaaactg cccagcatgc cgctatcgga aatgtcttca ggctggaatg 2280

aaccttgaag ctcgaaaaac aaagaaaaaa atcaaaggga ttcagcaagc cactgcagga 2340

gtctcacaag acacttcgga aaatcctaac aaaacaatag ttcctgcagc attaccacag 2400

ctcaccccta ccttggtgtc actgctggag gtgattgaac ccgaggtgtt gtatgcagga 2460

tatgatagct ctgttccaga ttcagcatgg agaattatga ccacactcaa catgttaggt 2520

gggcgtcaag tgattgcagc agtgaaatgg gcaaaggcga tactaggctt gagaaactta 2580

cacctcgatg accaaatgac cctgctacag tactcatgga tgtttctcat ggcatttgcc 2640

ttgggttgga gatcatacag acaatcaagc ggaaacctgc tctgctttgc tcctgatctg 2700

attattaatg agcagagaat gtctctaccc tgcatgtatg accaatgtaa acacatgctg 2760

tttgtctcct ctgaattaca aagaatgcag gtatcctatg aagagtatct ctgtatgaaa 2820

accttactgc ttctctcctc agttcctaag gaaggtctga agagccaaga gttatttgat 2880

gagattcgaa tgacttatat caaagagcta ggaaaagcca tcgtcaaaag ggaagggaac 2940

tccagtcaga actggcaacg gttttaccaa ctgacaaagc ttctggactc catgcatgag 3000

gtggttgaga atctccttac ctactgcttc cagacatttt tggataagac catgagtatt 3060

gaattcccag agatgttagc tgaaatcatc actaatcaga taccaaaata ttcaaatgga 3120

aatatcaaaa agcttctgtt tcatcaaaaa tga 3153

<210> 67
<211> 1052
<212> PRT
<213> Saccharomyces cerevisiae

<400> 67

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1 5 10 15

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
20 25 30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
35 40 45

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
50 55 60

Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln
65 70 75 80

Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro Gln Gly
85 90 95

Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly
100 105 110

Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu Asn Asp
115 120 125

Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu
130 135 140

Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys
145 150 155 160

Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser
165 170 175

Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu Glu Pro
180 185 190

Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr Glu Glu

```
        195                 200                 205

Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu Ser Thr
    210                 215                 220

His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu Ile Lys
225                 230                 235                 240

Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp Pro Arg Met
                245                 250                 255

Asp Ser Lys Glu Ser Leu Ala Pro Pro Gly Arg Asp Glu Val Pro Gly
            260                 265                 270

Ser Leu Leu Gly Gln Gly Arg Gly Ser Val Met Asp Phe Tyr Lys Ser
        275                 280                 285

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Val
    290                 295                 300

Ala Ala Ala Ser Gln Ala Asp Ser Lys Gln Gln Arg Ile Leu Leu Asp
305                 310                 315                 320

Phe Ser Lys Gly Ser Thr Ser Asn Val Gln Gln Arg Gln Gln Gln Gln
                325                 330                 335

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro
            340                 345                 350

Gly Leu Ser Lys Ala Val Ser Leu Ser Met Gly Lys Tyr Met Gly Glu
        355                 360                 365

Thr Glu Thr Lys Val Met Gly Asn Asp Leu Gly Tyr Pro Gln Gln Gly
    370                 375                 380

Gln Leu Gly Leu Ser Ser Gly Glu Thr Asp Phe Arg Leu Leu Glu Glu
385                 390                 395                 400

Ser Ile Ala Asn Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys
                405                 410                 415

Ser Ser Thr Ser Ala Thr Gly Cys Ala Thr Pro Thr Glu Lys Glu Phe
            420                 425                 430

Pro Lys Thr His Ser Asp Ala Ser Ser Glu Gln Gln Asn Arg Lys Ser
        435                 440                 445
```

```
Gln Thr Gly Thr Asn Gly Gly Ser Val Lys Leu Tyr Pro Thr Asp Gln
    450                 455                 460

Ser Thr Phe Asp Leu Leu Lys Asp Leu Glu Phe Ser Ala Gly Ser Pro
465                 470                 475                 480

Ala Ser Lys Asp Thr Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile
                485                 490                 495

Asp Glu Asn Leu Leu Ser Pro Leu Ala Gly Glu Asp Asp Pro Phe Leu
            500                 505                 510

Leu Glu Gly Asn Thr Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp
        515                 520                 525

Thr Lys Pro Lys Ile Lys Asp Thr Gly Asp Thr Ile Leu Ser Ser Pro
    530                 535                 540

Ser Ser Val Ala Leu Pro Gln Val Lys Thr Glu Lys Asp Asp Phe Ile
545                 550                 555                 560

Glu Leu Cys Thr Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Pro Val
                565                 570                 575

Tyr Cys Gln Ala Ser Phe Ser Gly Thr Asn Ile Ile Gly Asn Lys Met
            580                 585                 590

Ser Ala Ile Ser Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr
        595                 600                 605

His Tyr Asp Met Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys
    610                 615                 620

Pro Val Phe Asn Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp
625                 630                 635                 640

Asn Arg Cys Gln Gly Ser Gly Glu Asp Ser Leu Thr Ser Leu Gly Ala
                645                 650                 655

Leu Asn Phe Pro Gly Arg Ser Val Phe Ser Asn Gly Tyr Ser Ser Pro
            660                 665                 670

Gly Met Arg Pro Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Ala Ala
        675                 680                 685

Thr Gly Pro Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser
    690                 695                 700
```

```
Gly Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe
705                 710                 715                 720

Lys Arg Ala Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn
                725                 730                 735

Asp Cys Ile Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg
            740                 745                 750

Tyr Arg Lys Cys Leu Gln Ala Gly Met Ala Asn Leu Glu Ala Arg Lys
        755                 760                 765

Thr Lys Lys Lys Ile Lys Gly Ile Gln Gln Ala Thr Ala Gly Val Ser
    770                 775                 780

Gln Asp Thr Ser Glu Asn Pro Asn Lys Thr Ile Val Pro Ala Ala Leu
785                 790                 795                 800

Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro
                805                 810                 815

Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Ala Trp
            820                 825                 830

Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala
        835                 840                 845

Ala Val Lys Trp Ala Lys Ala Ile Leu Gly Leu Arg Asn Leu His Leu
    850                 855                 860

Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala
865                 870                 875                 880

Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser Ser Gly Asn Leu Leu
                885                 890                 895

Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Ser Leu Pro
            900                 905                 910

Cys Met Tyr Asp Gln Cys Lys His Met Leu Phe Val Ser Ser Glu Leu
        915                 920                 925

Gln Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu
    930                 935                 940

Leu Leu Leu Ser Ser Val Pro Lys Glu Gly Leu Lys Ser Gln Glu Leu
945                 950                 955                 960
```

```
Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile
                965                 970                 975

Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln
            980                 985                 990

Leu Thr Lys Leu Leu Asp Ser Met  His Glu Val Val Glu  Asn Leu Leu
        995                 1000                1005

Thr Tyr  Cys Phe Gln Thr Phe  Leu Asp Lys Thr Met  Ser Ile Glu
    1010                1015                1020

Phe Pro  Glu Met Leu Ala Glu  Ile Ile Thr Asn Gln  Ile Pro Lys
    1025                1030                1035

Tyr Ser  Asn Gly Asn Ile Lys  Lys Leu Leu Phe His  Gln Lys
    1040                1045                1050
```

<210> 68
<211> 158
<212> PRT
<213> Saccharomyces cerevisiae

<400> 68

```
Met Ser Thr Val Pro Leu Val Tyr Ser Pro Val Asp Arg Glu Pro Leu
1               5                   10                  15

His Asp Asn Ser Ala Asn Ile Lys Arg Pro Leu Gly Ser Phe Val Thr
            20                  25                  30

Ser Ser Ala Ala Cys Phe Lys Pro Leu Thr Ile Pro Gly Pro Thr Thr
        35                  40                  45

Pro Cys Ala Phe Val Met Ser Ala His Ser Ala Ile Leu Tyr Thr Pro
    50                  55                  60

Ala Glu Tyr Cys Asn Leu Thr Val Leu Pro Met Ser Ala Asn Phe Leu
65                  70                  75                  80

Ser Ser Lys Ser Lys Lys Leu Tyr Leu Ala Asp Asn Ala Phe Ser Gly
                85                  90                  95

Leu Thr Val Pro Ser Met Glu Lys Ser Val Lys Ile Ser Thr Cys Val
            100                 105                 110

Phe Ser Lys Gln Ile Leu Gly Pro Asn Ala Ser Thr Asn Ser Ser Asn
        115                 120                 125
```

Ser Leu Val Val Arg Thr Ser Asn Glu Ala His Lys Phe Val Cys Phe
130 135 140

Ser Cys Met Ile Leu Asn Ser Leu Ala Ala Thr Gly Leu Gly
145 150 155

<210> 69
<211> 267
<212> PRT
<213> Saccharomyces cerevisiae

<400> 69

Met Ser Lys Ala Thr Tyr Lys Glu Arg Ala Ala Thr His Pro Ser Pro
1 5 10 15

Val Ala Ala Lys Leu Phe Asn Ile Met His Glu Lys Gln Thr Asn Leu
20 25 30

Cys Ala Ser Leu Asp Val Arg Thr Thr Lys Glu Leu Leu Glu Leu Val
35 40 45

Glu Ala Leu Gly Pro Lys Ile Cys Leu Leu Lys Thr His Val Asp Ile
50 55 60

Leu Thr Asp Phe Ser Met Glu Gly Thr Val Lys Pro Leu Lys Ala Leu
65 70 75 80

Ser Ala Lys Tyr Asn Phe Leu Leu Phe Glu Asp Arg Lys Phe Ala Asp
85 90 95

Ile Gly Asn Thr Val Lys Leu Gln Tyr Ser Ala Gly Val Tyr Arg Ile
100 105 110

Ala Glu Trp Ala Asp Ile Thr Asn Ala His Gly Val Val Gly Pro Gly
115 120 125

Ile Val Ser Gly Leu Lys Gln Ala Ala Glu Glu Val Thr Lys Glu Pro
130 135 140

Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Cys Lys Gly Ser Leu Ser
145 150 155 160

Thr Gly Glu Tyr Thr Lys Gly Thr Val Asp Ile Ala Lys Ser Asp Lys
165 170 175

Asp Phe Val Ile Gly Phe Ile Ala Gln Arg Asp Met Gly Gly Arg Asp
180 185 190

```
Glu Gly Tyr Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp Asp
        195                 200                 205

Lys Gly Asp Ala Leu Gly Gln Gln Tyr Arg Thr Val Asp Asp Val Val
    210                 215                 220

Ser Thr Gly Ser Asp Ile Ile Ile Val Gly Arg Gly Leu Phe Ala Lys
225                 230                 235                 240

Gly Arg Asp Ala Lys Val Glu Gly Glu Arg Tyr Arg Lys Ala Gly Trp
                245                 250                 255

Glu Ala Tyr Leu Arg Arg Cys Gly Gln Gln Asn
            260                 265
```

<210> 70
<211> 286
<212> PRT
<213> Saccharomyces cerevisiae

<400> 70

```
Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1               5                   10                  15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
            20                  25                  30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
        35                  40                  45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
    50                  55                  60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65                  70                  75                  80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
                85                  90                  95

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
            100                 105                 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
        115                 120                 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
    130                 135                 140
```

```
Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
145                 150                 155                 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
                165                 170                 175

Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
            180                 185                 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
        195                 200                 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
    210                 215                 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
225                 230                 235                 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
                245                 250                 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
            260                 265                 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
        275                 280                 285
```